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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model Run on: March 21, 2004, 02:21:01; Search time 12121 Seconds (without alignments) (without alignments)	US-09-817-198C-1 1257 1 tgcccgctgcccgcagaaaaaaaaaaaaaaaaaa 3257	IDENTITY NUC Gapop 10.0 , Gapext 1.0
OM nucleic - nuo Run on:	Title: Perfect score: Sequence:	Scoring table:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

3470272 segs, 21671516995 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries GenEmbl: Database :

gb ba: *
gb ba: *
gb ba: *
gb ov : * *
gb br: *

em_htgo_hum:* em_htgo_mus:* em_htgo_other:* em_htg_hum:*
em_htg_inv:*
em_htg_other:*
em_htg_mus:* em_htg_pln:*
em_htg_rod:*
em_htg_mam:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Scor	a	% Query Match	Length	DB	ID	Description
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П	3030.	C)	۳.		٠.	BC040679	0679 Homo B
7	2696.	9	82.8	5		CNS01DX4	2 Human
m	23	60	· .		6	HSM806937	Homo a
4	3	α	36.6		_	AX347040	Segne
· LC	2	- α				AX348456	
	.0	00	35.6		_	AX347041	
0	1160.	60	'n		9	AX348457	AX348457 Sequence
	2	~	ö			AX399903	_
თ	99	~			9	AX014147	
10	99	۲,	ė.			BD205055	Humar
11	8	<u>~</u>	'n.			BC027769	
12	9	Ω,	٠ م		<u>.</u>	AX781147	AX781147 Sequence
E :	577.	۰۰	· •			RATRABISX	M83679 Sprague-Daw
	477	4.0	4.		-	AX396088	AX396088 Sequence
5 1.5	458	ט פ				AX334820	AASS#820 Sequence
17	416.	5 4		4		BC013790	BC013790 Mus muscu
18	38	<u>.</u>	11.8		9	AX779778	duence
19	378.	4	ä	5		AC132331	is mus
50	338.	N,	٠			BC063736	endous
21	234	<u>,</u>	ο τ 4 τ	313	ه م	AX341683 BC002977	AX341683 Sequence
2 6	234	40				BC002377	AKO25165 Homo Bapi
24	9 6	ı v				S53268	S53268 Homo sapien
52	22	6				AF498943	AF498943 Homo sapi
56	22	6	•			BT007184	BT007184 Homo sapi
27	55	6	•			BT008275	BT008275 Synthetic
2 6	22.5	D <	•		ۍ د د	HSMRAB8 SE3370	X56741 H. sapiens m
9.0	224	r (\)				BC019990	BC019990 Mus muscu
31	222					CFRABB	X56385 Canine rab8
32	218	7	•			DYGORA2	M38391 Discopyge o
33	217.	ω.	٠			AX236078	AX236078 Sequence
34	217.	œ, α			σ,	BC020654	BC020654 Homo sapi
35	217	20 0	•			AA235U/5	AAZ360/6 Sequence
3.5	217	0 00	•			AB038333 AX285074	AX285074 Semience
38	217.	0				AX285080	AX285080 Sequence
39	217.	89	•			AX285089	AX285089 Sequence
40	217.	80	•		_	AX285091	91
41	217.	80	•		_	AX876024	5024
42	217.	ω,	6.7		_	BD155904	904 Primer f
43	217	.	•		•	AKGOILII	1111
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						ALIGNMENTS	
RESULT 1							
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rocus		3C04	BC040679			6 bp mRNA	r PRI 11-D
DEFINITION		OHOP CUCY	8ap1	INB RA	7.	member RAS onocogene ra	ramily, mkna (cuna clone
ACCESSION		3004	BC040679	=	100	td	
VERSION		3C04	0679.		GI:347833	346	
KEYWORDS		MGC.	200		(human)		
ORGANISM		Homo			llan)		
			•	Motor		Warney Cranists Vor	toberts. Entelegetomi.

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates; Catarrhini, Hominidae; Homo.
1 (bases 1 to 33.2)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., REFERENCE AUTHORS

Gaps

Length 3326;

9

220

JOURNAL

REMARK COMMENT

240 340

280

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361 AGAGGGGCTCACCGGGGAAGGCAAGGCGAGGGCAGATGGGAAGGCAAATGCTTCCAG 420
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              26. .343
/note="RAB; Region: Rab subfamily of small GTPases"
/db_xref="CDD:cd00154"
                                                                                                                                                                                                            8; Indels 132;
                                                                                                                                                         DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 CATGAAGTGGGTCAGTGACGTGGATGA-------
                                                                                                                                                   Score 3030.2;
Pred. No. 0;
0; Mismatches
                                                                                                                                                      93.0%;
95.8%;
                                                                                                                                                                                                            Matches 3187; Conservative
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Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatcherko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Mokernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, K., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butferfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 70 Row: p Column: 2.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /trānslation="MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVD
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VSDVDEVGDATSLFGCGEGASPGKARGPDGKANASRKLCLPQPWKTSGTHQKASRR
SLLGIRLMRSRNGRWEESKGSSWRRSWAWTSMKQVPAPTSTLKSHSRV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       info@bogsc.bc.complete Asano, Isn Bosdet, Yaron Butterfield; Steven Jones, Jennifer Asano, Isn Bosdet, Yaron Butterfield; Steven Jones, Jennifer Asano, Isn Bosdet, Yaron Butterfield; Susanna Chai, Readman Chiu, Chris Pjell, Erin Garland, Ran Guin, Letticia Heiso, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvanch Sacedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Teai, Natasia van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submitted (29-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
On Sep 16, 2003 this sequence version replaced gi:26251822.
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/db_xref="G1:34783347"
/db_xref="I_AAH40578.2"
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/clone_lib="NIH_MGC_95"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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'gene="RAB15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
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REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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540 509 9 569 720 689 780 749 840

CDS

FEATURES

us-09-817-198c-1.rge

/mol_type="genomic DNA" /db xref="taxon:9606" /chromosome="14" /clone="R-840119" /clone="R-840119" /clone="matching EMBL:H99639 Rudo: 2216322307 /note="matching EMBL:H99639 Rudo: 3.86849 Identified using the e-PCR software (G. Schuler)" 30401. 30624 /note="matching EMBL:R42375 Rudo:RH69913 dbgr3:ST849990 Identified using the e-PCR software (G. Schuler)" Identified using the e-PCR software (G. Schuler)"	e-FCR Software (G. Schuler) Z39082 e-PCR Software (G. Schuler) e-PCR Software (G. Schuler)	dbsT6:ST32000 dbsT6:ST32013 Identified using the e-PCR software (G. Schuler) " 4471244832 /note="matching EMBL:L00635 RHdb:RH53755 dbsT8:ST31241 Identified using the e-PCR software (G. Schuler) " 4722247411 /note="matching EMBL:AA165116	RHdb:RH48540 dbSTS:ST24159 Identified using the e-PCR software (G. Schuler) " 128322128437 /notee=marching EMBL:G07650 RHdb:RH34434 dbSTS:STS6376 Identified using the e-PCR software (G. Schuler) " 164135164257 /notee=marching EMBL:AA160869		RHdb:RH10964 dbSTS:STS1017 Identified using the e-PCR software (G. Schuler)" 173564173713 /note="matching EMBL:R10900 RHdb:RH53901 dbSTS:STS2552 Identified using the e-PCR software (G. Schuler)"	EMBL:G27797 the e-PCR software (G. re 2696.6; DB 9; Lengt
STS STS	STS STS	STS STS	STS STS	STS STS	STS	STS ORIGIN Query Match
Db 3120 TCGTCACCACCTCTGCACCTGTGTGTTTTGAGACTCCATCCA	RESULT 2 CNSO1DX4 LOCUS LOCUS DEFINITION Human chromosome 14 DNA sequence BAC R-840119 of library RPCI-11 From chromosome 14 of Homo sapiens (Human), complete sequence. AL139022.4 GI:14148954 KESYMORDS HTG. SOURCE HTG. ORGANISM HTG. ORGANISM Ebkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.	REFERENCE 1 (bases 1 to 190517) AUTHORS Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Brottier,P., Cattolico,L., Barbe,V., Pelletier,B., Artiguenave,F., Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Gyapay,G., Saurin,W. and Weissenbach,J. TITLE Sequencing of the human chromosome 14 JOURNAL Unpublished REFERENCE 2 (bases 1 to 190517) AUTHORS Genoscope.	Į.	The following BAC sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end) : C-2509G16 (AC=AL355076) Downstream BAC (overlapping the SP6 end) : C-2300N4		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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/product=npothetical protein"
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/gene="DKFZp686J06205"
/note="eimilarity to GTP-binding protein rabl5 (Rattus</pre>
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Best Local Similarity 99.2%; Pred. No. 0;
Matches 1431; Conservative 0; Mismatches 12; Indels 0;
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/db_xref="taxon:9606"
/map="14q23.3"
/clone="DKFZp686J06205"
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Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s. wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
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1 (bases 1 to 2210)

Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.

The German Human cDNA Consortium
Direct Submission
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BX640825
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/organism="Homo sapiens"

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DNA

AX348456 7924 bp I Sequence 151 from Patent W002028806.

RESULT 5
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1635 1755 TITAAGACAAAGCGCTCATCTTGCCCTCTACCTCCTGATAGGCTTGAGGGTTTGCCAACC 2055 1455 1756 CCAGGGACAGCAGTTTGCACAGCAGAGGGGAATGTAGCAACAGCAGGGCCTCCTAGGCCC 1815 ö 420 480 541 TATTTTTTATTTTTAGGTAAGAGAGTATTTTTTAGATTTTTAGGCGGAGGATTGAGT 600 601 Tragtritragtaartaaggritritrigggartraaagritrafggaagggaagaggaa 660 Olek,A., Piepenbrock,C. and Berlin,K.
Method and nucleic acids for pharmacogenomic methylation analysis
Patent: WO 0202806-A 151 10-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
1. .7924
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/mol_type="unassigned DNA"
/db_xref="texon:32630"
/note="chemically treated genomic DNA (Homo sapiens)
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Diagnosis of diseases associated with the immune
Patent: Wo 0200928-A 2112 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
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Method and nucleic acids for pharmacogenomic methylation analysis
Patent: Wo 0202806-A 152 10-JAN-2002;
Epigenomics AG (DB)
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/organism="synthetic construct"
/mol.type="unassigned DNA"
/db xref="texon:32630"
/noTe="chemically treated genomic DNA (Homo sapiens)"
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Best Local Similarity 74.1%; Pred. No. 1.7e-279;
Matches 1468; Conservative 0; Mismatches 512;
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Sequence 152 from Patent W00202806. 
AX348457.1 GI:18614493
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Patent: WO 0218424-A 74 07-MAR-2002;
HYSEQ, INC. (US)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                TTTCTCTCCTAGCCCCCTCAGGAAGAAGACTATATTTGTACTGTACCTAGGGGFTCT
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                    Schmitt, A., Specht, T., Dahl, E., Hinzmann, B., Rosenthal, A. and Pilarsky, C.
Human nucleic acid sequences of bladder tumour tissue
Patent: WO 9954417-A 12 28-0CT-1999,
SCHMITT ARIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN (DE); PILARSKY CHRISTIAN (DE)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                           Indels
                              4
Pred. No. 2.3e-239;
0; Mismatches 4;
  99.68;
                         Matches 1002; Conservative
  Best Local Similarity
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Mus musculus RAB15, member RAS oncogene family, mRNA (cDNA clone MGC:38375 IMAGE:5345297), complete cds.
BC027769.1 GI:20380721
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Bases I to 3139)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Rlausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.E., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
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                                                                                                                                      TGGGACTCCTTGGGTATCAAGACCTATGCCACATCACACTGGGGCTAGGGAAGTAGGTGA 2657
                                                                                                                                                                                                                               TGCCAGCCCTCAAGTCTGTCTTCAGCCAGGGACTTGAGAAGTTATATTGGGCAGTGGCTC 2717
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AUTHORS
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ANDRE ROSENTHAL
C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61K48/00, A61P13/10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-APR-1999 JP 2000544779
21-APR-1998 DE 198 18 619.3
THOWAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12P21/08, C12Q1/68, PC
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 895)
Specht, T., Hinzmann, B., Schmitt, A., Pilarsky, C., Dahl, E. and Rosenthal, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Human nucleic acid sequence originating in cystic cancer tissue Parent: JP 2002512023-A 9 23-APR-2002;
METAGEN GESELLSCHAFT FUER GENOM FORSCHUNG MBH
OS Homo sapiens (human)
PN JP 2002512023-A/9
PD 23-APR-2002
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                                                                                                                          GCACGCCACCTGCTCCTGACCTCCACTATCTCCCCTGTGACGGGGAACTTCGTGTACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2358 AGAACCTCACTTCCTTACTCCTCCAAAAAGAAGTGGGGAAAGAACCATCAAACCTTTCCT
    GCACGCCACCTGCTCCTGAGCCTCCACTATCTCCCTGTGACGGGTGAACTTCGTGTACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.6%; Score 866.2; DB 6; Length 895; 99.5%; Pred. No. 8.9e-206; ive 0; Mismatches 3; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism='Homo sapiens (human)'.
                                                                                                                                                                                                                                                                               Location/Qualifiers
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/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002512023-A/9.
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BD205055
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Pred. No. 2.4e-192;
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                                                                       Query Match 25.0%;
Best Local Similarity 67.4%;
Matches 1662; Conservative
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Tissue Procurement: Jeffrey Green M.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter, N. Ayele, K. Becketrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Blakesley, R.W., Ganante, S., Guan, X., Gupta, J., Haghighl, P.,
Bansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q. L., Masiello, C., Maskeri, B., Mastrian, S. D., McCloskey, J. C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 55 Row: d Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19527265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="LocusID:104886"
/translation="WAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVD
FKWKTIDVDDSIKVRIQIWDTAGQERVQTTKQYYRRAQGIFLVVDISSERSYQHIMKW
VSDVDEYAPEGVQVLIGUKADEBEGKRQVGREGGGQLAKEYGHDFTSACTVLNIKE
SFTRLTELVLQAHRKELDGLRTRASNELALAELEEDEGKFEGPANSSKTCWC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="Mammary tumor. C3(1)-Tag model. Infiltrating
Juctal Carcinoma. 5 month old virgin mouse."
McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S., Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W., Worllay, N. C., Hale, S., Garcia, A. M., Gay, L. J., Lu, X., Gibbs, R. A., Sudergen, E. J., Lu, X., Gibbs, R. A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y., Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D., Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smallus, D. E., Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229. .720
/note="RAB; Region: Rab subfamily of small GTPases
                                                                                                                                                                                                                                                    human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/product="Rabl5, member RAS oncogene family"
/protein_id="AAH27769.1"
/db_xref="GI:20380722"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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/clone="MGC:38375 IMAGE:5345297"
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/db_xref="MGI:1916865"
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/organism="Mus musculus"
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/clone lib="NCI CGAE
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/strain="FVB/N"
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Direct Submission
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1124 ACGACGGTCAAGGCTGAAGGCCACTTCAAGATTCCTTAGTGCATCTCGT 1177 1040 CTCTTCTCTCTCTCTCTCCCCACTTCTTTCTCTTAGTGCATCTCGTG 1099 1178 GGGCTCTCTGCTTTTTCTCTTTCTTTTCTTTCTTCTCTCCCCCC	CTGCCTCTTGGGGAACTGAGGCAGGCACGCAGAGAAAGGAAAACAAAAAAAA

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/translation="MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVD
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VSDVDEYAPEGVQKILIGHKADEREQKRQVBEQGQQLAKEYGMPFETSACTRLNIKE
SFTRLFELVLQAHRKELDGLRYCASNELALAELEEDBGKTEGPANSSKTCWC"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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241 TATTTGTACTGTACCCTAGGGGTTCTGGAAGGGAAACATGGAATCAGGATTCTATAGAC
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Sprague-Dawley (clone LRB9) RAB15 mRNA, complete cds.
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rabls, a novel low molecular weight GTP-binding
specifically expressed in rat brain
J. Biol. Chem. 267 (9), 5768-5775 (1992)
92210533
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/mol_type="mRNA"
/strain="Sprague-Dawley"
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'tissue_lib="LAMBDA_ZAPII"
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/product="RAB15"
/protein_id="AAA41995.1"
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LMW GTP-binding protein.
Rattus norvegicus (Norway
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Compositions and methods for the therapy and diagnosis of colon
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14.7%; Score 477.4; DB 6;
Best Local Similarity 99.4%; Pred. No. 2.6e-108;
Matches 478; Conservative 0; Mismatches 3;
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Patent: WO 0194629-A 5329 13-DEC-2001;
Avalon Pharmaceuticals (US)
              cancer Patent: WO 0212328-A 303 14-FEB-2002; CORIXA CORPORATION (US) Location/Qualifiers
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    .481
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

    .463
/organism="Homo sapiens"

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                                                                                                         Length 463;
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                                                                                                       Query Match 13.5%; Score 438.8; DB 6; Best Local Similarity 99.3%; Pred. No. 1.2e-98; Matches 451; Conservative 0; Mismatches 2;
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Search completed: March 21, 2004, 08:59:33 Job time : 12136 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

March 21, 2004, 02:17:36; Search time 1147 Seconds (without alignments) 12063.105 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

6747726 Total number of hits satisfying chosen parameters: 3373863 seqs, 2124099041 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_29Jan04:* Database

geneseqn2001as:* geneseqn1980s:* geneseqn1990s:* geneseqn2000s:*

geneseqn2003bs:* geneseqn2004s:

geneseqn2003as:*

geneseqn2002s:*

geneseqn2001bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Aad47168 Human Ras	Aak82285 Human imm	Human	Human	Abk40069 Human che	Abl34138 Human imm	Abk40070 Human che	Abl34139 Human imm	Aas27053 cDNA enco	Adb93231 Human cDN	Abq93361 Human cDN	Aaz24400 Human bla	Aas27472 cDNA enco	Adb93650 Human cDN	Abk44752 cDNA enco	Abl66992 Thyroid c	Ach33636 Human end	Aat25457 Human gen	Human	Aba09160 Human rab	Abq54410 Human ova	Aah75182 Nucleotid	Abv78060 Hypoxia-r
		ΙD	AAD47168	AAK82285	AAD47169	AAC75813	ABK40069	ABL34138	ABK40070	ABL34139	AAS27053	ADB93231	ABQ93361	AAZ24400	AAS27472	ADB93650	ABK44752	ABL66992	ACH33636	AAT25457	ABL38341	ABA09160	ABQ54410	AAH75182	ABV78060
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de	Query	Match	100.0	82.8	82.8	48.1	36.6	36.6	35.6	35.6	35.6	35.6	30.7	26.6	16.4	16.4	14.7	13.5	13.0	9.6	9.4	7.0	7.0	6.7	6.7
		Score	3257	2696.6	2696.6	1568.2	1192.8	1192.8	1160.8	1160.8	1160.6	1160.6	1000.2	866.2	534.2	534.2	477.4	438.8	424.4	313.4	307	.229	228.4	217.8	217.8
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1 AAS60878 1 AAS60884 1 AAS60893	AAS60895 ABV25781	5 ABV30037 1 AAH13912	1 AAH04301 3 ADB12721	9 ADB52880	3 AAC01700 3 AAA40104	3 AAA40108	AAF16196	AAH17889	AAS71453 ABL29661	5 ABX04179	3 AAA40109	3 AAF18072	5 AAS87552
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217.8	217.8	217.8 217.8	214.2	203.2	202.6 200.2	200.2	198.4	198.4	196.8 196.6	195.6	195.2	192	188.6
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ALIGNMENTS

AAD47168 standard; cDNA; 3257 BP. (first entry) 24-FEB-2003 AAD47168; AAD47168

RESULT 1

Human Ras-like protein encoding cDNA

Human; Ras-like protein; inflammation; cell proliferation; apoptosis; immunodeficiency; neurodegenerative; Alzheimer's disease; cirrhosis; parkinson's disease; wasting disease; cachexia; myocardial infarction; osteoporosis; atherosclerosis; glomerulonephritis; crohn's disease; irritable bowel syndrome; multiple sclerosis; osteoparthritis; allergy; pancreatitis; autoimmune thyroiditis; rheumatoid arthritis; osteopathic; pancreatitis; autoimmune thyroiditis; rheumatoid arthritis; osteopathic; neuroprotective; vasotropic; cytostatic; dermatological; nephrotropic; ophthalmological; tranquilliser; cancer; stroke; Grave's disease; AIDS; asthma; anaemia; drug screening; gene; ss.

Homo sapiens

"Human Ras-like protein" Location/Qualifiers 45. .683 /*tag= b /product= " 684. .3257 /*tag= c ø ...44 *tag= Key 5'UTR 3'UTR CDS NAME OF STREET O

WO200277193-A2.

03-OCT-2002.

27-MAR-2002; 2002WO-US009328.

27-MAR-2001; 2001US-00817198.

(PEKE) PE CORP.

Ye J, Di Francesco V, Beasley EM; 3an W,

WPI; 2003-018913/01. P-PSDB; AAE29096.

New isolated human Ras-like protein polypeptide, useful for diagnosing, treating or preventing inflammation and disorders associated with cell proliferation and apoptosis, e.g. AIDS, cancer, allergies, anemia, asthma corresponding relates to human Ras-like protein and its Claim 4; Page 73-74; 82pp; English invention or stroke.

nucleic acid. The Ras-like protein and DNA is useful in the development of human therapeutics and diagnostic compositions. They are useful in the diagnosis, prevention and treatment of infolammation and disorders associated with cell proliferation and apptosis, e.g. AIDS and other infectious or genetic immunodeficiencies, neurodegenerative disease e.g. Alzheimer's disease, Parkinson's disease, washing disease e.g. cachaxia, ischaemic injuries e.g. myocardial infarction, stroke or reperfusion injury, toxin-induced diseases such as alcohol-induced liver damage or injury, toxin-induced diseases such as alcohol-induced liver damage or injury, toxin-induced diseases such as alcohol-induced liver damage or injury, toxin-induced diseases such as alcohol-induced liver damage or injury, toxin-induced diseases such as alcohol-induced liver damage or associated with inflammation including allergies, atopic dermatitis, atherosclerosis, asthma, anaemia, crohn's disease, diabetes mellitus, atherosclerosis, allemation including allergies, atopic dermatitis, untiple sclerosis, osteoarthritis, pandrome, lupus erythematosus, multiple sclerosis, osteoarthritis, pandrome, uveitis, rauma, or viral, bacterial, fungal, parastic, protozoal or helminthic infections. The antibodies of the invention are useful in pharmacogenomic analysis or for tissue typing. The transgenic animals are useful for studying the function of a Ras-like protein, and identifying and evaluating assays and its activity. Ras-like protein is used in drug screening assays and its bNA is used in gene therapy. The present esquence is human Ras-like protein agence of human encoding cDNA

Sequence 3257 BP; 793 A; 892 C; 870 G; 702 T; 0 U; 0 Other;

ö 180 240 120 120 240 300 360 420 420 480 480 540 540 121 GCGGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTA 180 9 9 ACTTCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAGTCATTCACGCGTCTGA TGCCCGCTGCCCGCCGCAGTTCCCCGCCCGCTGGCCCCAGTCATGGCGAAGCAGTACG rececercecececesaries de construir de la constr Archicerorrected arcases de la constant de la consta GCCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTA AGATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAGATCTGGGACACTGCAG AGATGAAGACCATAGAGGTAGACGCATCAAAGTGCGGATACAGATCTGGGACACTGCAG 241 GGCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGGATATTTT TGGTCTATGACATTAGCAGCGAGCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACG TGGATGAGTACGCACCAGAAGGCGTCCAGAAGATCCTTATTGGGAATAAGGCTGATGAGG AGCAGAAACGCCAGGTGGGAAGAGAGCAAGGGCAGCTGGCGGAGGAGTATGGCATGG AGCAGAAACGCCAGGTGGGAAGAGAGCAAGGCCAGCAGCTGGCGAAGGAGTATGGCATGG ACTICIAIGAAACAAGIGCCIGCACCAACCICAACAITAAAGAGICATICACGCGICIGA Gaps ö Query Match
100.0%; Score 3257; DB 7; Length 3257;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3257; Conservative 0; Mismatches 0; Indels 0; 7 61 61 121 181 181 241 301 301 361 421 361 421 481 181 a à ઠે 유 ò 셤 ò 셤 ò 쉽 8 9 ò g 8 원

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Db 2701 ATATTGGGCATTCCTTCTCTCTCTCTCTCTGCATACTTCCTCGAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	RESULT 2 AAK82285/c ID AAK82285 standard, DNA; 3240 BP. XX AC AAK82285 standard, DNA; 3240 BP. XX DT 07-NOV-2001 (first entry) XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37097. XX KW Human; immune; haematopoietic, immune/haematopoietic antigen; cancer; XX KW CLOSTABLE; gene therapy; vaccine; metastasis; ds. XX NO 99-AUG-2001. XX

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2000US-0231413P

2000US-0231414P

2000US-0232081P

2000US-023238P

2000US-023239P

2000US-023239P

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2000US-023239P

2000US-0232400P

2000US-0232400P

2000US-0232401P

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2000US-023424P

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13-OCT-2000;
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20-OCT-2000; 2000US-0241826P.
08-NOV-2000; 2000US-024647P.
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08-NOV-2000; 2000US-024647P.
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08-NOV-2000; 2000US-024652P.
08-NOV-2000; 2000US-024651P.
08-NOV-2000; 2000US-024920P.
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HUMAN GENOME (HUMA-) Ruben SM Barash SC, Rosen CA,

NPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 37097; 3071pp + Sequence Listing; English

amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to polymucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the

8 B 8 B 8 B 8 B 8 B 8 B

OS Homo sapiens.	2572 FH Key Location/Qualifiers 2572 FT variation replace(206, -) FT /*tag= a /*tag= a /*tag= nucleotide nolymorphism"	FT CDS 204425772 FT /*tag= b // product= "Human Ras-li	exon	FT variation FT	variation I	variation r	/_tdg= n /standard name= "Single nucleotide variation replace(13781,C) /*tag= i	<pre>/standard name= variation replace(14050,C /*tag] /*tame= /standard name=</pre>	variation replace(14273, - / trag = k / standard name= variation replace(17582,C)	/*tag= 1 /standard_name= "Single nucleotide variation replace(17700,T) /*tag= m	variation r	PT variation replace(19328,T) (Atag= 0 FT / Atanged name= "Single nucleotide replace(19570,G)	FT /*tag= p / standard name= "Single nucleotide polymorphism" FT variation replace(20892,T) FT /*tag= q /*tag= q /*tag= q /*tag= q /*tag= polymorphism"	exon 215552 <u>1</u> 615 /*teg= r intron 2161622462 /*tag= 8	exon	/*tag= exon 22975.	FT intron		FT /*tag= FT exon 25393.	
	ACTICIARANTCACTGGCTAATGAGAAAAGGAGACAGCTAAACTCTAG		1000 INGGETGGGGGTAGGGAAGTAGGTGATGCCAGCCTCAAGTCTGTCT		2693 GAGAAGTTATATTGGGCAGTGGCTCCAATCTGTGGACCAGTATTTCAGCTTTCCCTGAAG 	2753 ATCAGGCAGGGGCCATTCATTGTCTTCTCCTAGCCCCCTCAGGAAAGAAGAACTAT	2813 ATTTGTACTGTACCCTAGGGGTTCTGGAAGGGAAAACATGGAATCAGGATTCTATAGACT 	2873 GATAGGCCCTATCCACAAGGGCCATGACTGGGAAAAGGTATGGGAGCAGAAGATTG 	2933 GGATTTTAGGGTGCAGCTCACCCTAAACTTTTGGTGGCCTGGGGCATGTCTTGAG	2993 GCCCAGACTGTTAAGCAGGCTCTGCTGGCCTGTTTACTCGTCACCTCTGCACCTGCTTGCT	3053 GTCTTGAGACTCCATCCAGCCCCAGGCACGCCACCTGCTCCTGAGCCTCCACTATCTCCCCACTTCAGACTCCAGCCCAGGCAGCCAGC	TGTGACGGGTGAACTTCGTGTACTCGGGTCCATATATGAA 	3173 CATCTATTITAAACACAGATGTTTACAAAATAAAGATTATTTCAAACCACC 3223 	LT 3 7169 AAD47169 standard, DNA, 28770 BP.	AAD47169;	24-FEB-2003 (first entry)	human kas-like protein encoding gene.	Human; Ras-like protein; inflammation; cell proliferation; apoptosis; immunodeficiency; neurodegenerative; Alzheimer's disease; cirrhosis; Parkinson's disease; wasting disease; cachexia; myocardial infarction; category, atherwalls.	irritable bowel syndrome; multiple sclerosis; osteoarthritis; aller, pancreatitis; autoimmune thyroiditis; rheumatoid arthritis; osteopai	Slogren's syndrome; intection; transgenic; gene therapy; nootropic; neuroprotective; vasotropic; cytostatic; defmatological; nephrotrop; ontrhalmological; transmillian; cander struke; Grand, dispans

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The invention relates to human Ras-like protein and its corresponding nucleic acid. The Ras-like protein and DNA is useful in the development of human therapeutics and diagnostic compositions. They are useful in the diagnosis, prevention and treatment of inflammation and disorders associated with cell proliferation and apoptosis, e.g. AIDS and other infectious or genetic immunodeficiencies, neurodegenerative disease e.g. Alzheimer's disease, Parkinson's disease, wasting diseases e.g. cachexia, control injuries e.g. myocardial infarction, stroke or reperfusion injury, toxin-induced diseases such as alcohol-induced liver damage or cirrhosis, osteoporosis or cancer. They are also used to treat disorders associated with inflammation including allergies, atopic dermatitis, atherosclerosis, asthma, anaemia, Crohn's disease, diabetes mellitus, graves eighease, glomerulomephritis, gout, irritable bowel syndrome, clupus erythematosus, multiple sclerosis, osteoarthritis, pancreatiis, autoimmune thyroiditis, rheumatoid arthritis, Sjogren's syndrome, clupus erythematosus, multiple sclerosis, osteoarthritis, gandrome, cuestul for studying the function of a Ras-like protein in udentifying and evaluating modulators of its activity. Ras-like protein is used in drug screening assays and its DNA is used in gene therapy. The present and characters in human Ras-like protein gene is located at New isolated human Ras-like protein polypeptide, useful for diagnosing, treating or preventing inflammation and disorders associated with cell proliferation and apoptosis, e.g. AIDS, cancer, allergies, anemia, asthma /*tag= ae /standard name= "Single nucleotide polymorphism" replace(28096,G) /standard_name= "Single nucleotide polymorphism" /*pplace(20467,G) /*tag= ah /standard_name= "Single nucleotide polymorphism" _name= "Single nucleotide polymorphism" /*tag= ad /standard_name= "Single núcleotide polymorphism" replace(28071,T) "Single nucleotide polymorphism Beasley EM Claim 4; Page 74-81; 82pp; English. /*tag= ac /standard_name= " replace(26472,G) name= replace (26465, A) $replace (2\overline{8}403,G)$ Ye J, Di Francesco V, 27-MAR-2002; 2002WO-US009328 27-MAR-2001; 2001US-00817198 /*tag= af /standard_n WPI; 2003-018913/01. variation

Sequence 28770 BP; 6592 A; 7315 C; 7655 G; 7208 T; 0 U; 0 Other;

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DB 7; Length 28770;

1553 à ö 532 TGGCATGGACTTCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAGTCATTCAC 0; Gaps 34; Indels 82.8%; Score 2696.6; 98.8%; Pred. No. 0; iive 0; Mismatches

26101 26221 26401 26581 26642 ACCTCCCATGCAGCATGAACACAATTTCTCTCCACCTGGCTCCCAATTTAAAGATGTGG 26701 25861 cricircaeccreirrececaeccaecciecraecaecececeaecarereceaaec 26041 1072 1132 26281 1252 26341 1312 1372 26461 1432 26521 1492 1552 26641 1612 25562 TGCCAGGGGAGAGAGAGACACTGGACTAACCTGTGCCCTTTGGTTTCCAGTCATTCAC 25621 AGCGAACTCTTCGAAAACCTGCTGGTGCTGAGTCCTGTGTGGGGCACCCCACACACGACACC 25801 CCGTGTGTCCTGCTGTGCAGCTCGCTCTTTCCTTCCTAAGCTATCCAAGGGGAT 1192 712 772 832 952 ACTGTCTCACCATCCCGCACCCACAGACAACAGCCAGGCTGGAGTCCAGGCCACTTTC CGTGGGTGGGCCAAAGGCTACAGGGTGCTTCTTCCTCTTCCCCCACCCCCACCCCTCTC CCTCTTCCCTCAGGAGGCCCGTGGGCAGACAGGGGGGGGCTTTGCCCTGCTGCTGT 25922 GAGCGGCTCTGCTCATCTCAAGCAGCCCCTGTCCCCAGCCCGTCCACCCTGGAGTGGT ACTGTCTCACCATCCCGCACCCACCAGACAACAGCCAGGCTGGAGTCCAGGCCACTTTC AGCTGCTTTTCTCCGTGCATCGTGTCTCTTCTCTCTGCTTTTTCTCTTCCCCCCACTTC Accrecativated and a second a seco TCTTTCTCTGACCCCTCCCCTCCGGTGCGTTTCGTATCAAAGCTCCTCAAACCCCCGTCCC CCGGGGGCCCGCCGCTGTGCCTCTTTCCTTCCTTAAGCTATCCAAGGGGAT ATGTGCCATGGGCCTGCCTCCCCAGTGACCTGCGAAAGTGGAGCATCGAGGTAGGAGGA GAGCTTTGCCCTTGCTTGGCTGCCCGCCTGCTCTTTGGGGGAACTGAGCTCAGAGGCAGG ACCTCCCATGCAGCATGAACACAATTTCTCTCCACCTGGCTCCCAAATTTAAAGATGTGG AGGGAACTCTTCGAAAACCTGCTGGTGCTGAGTCCTGTGTGGGGCACCCCACACGACACC CCTCTTCCCTCAGGAGGCCCGTGGGCAGACAGGGGAGCCGGGGCTTTGCCCCTGCTGT GAGCGGCTCTGCTGTCATCTCAAGCAGCCCCTGTCCCCCAGCCCGTCCACCCTGGAGTGGT CTTCTTCAGCCTGTTTCCCCAGGCCAGGCCTGCTACGACCCCCACGATGTGCCGCAAGC TCTTTCTCTGACCCCTCCCCTCCGGTGCGTTTCGTATCAAAGCTCCTCAAACCCCCGTCCC GGACCCAGGCTCGTGGGGAGGTTCCACCCTTGGATCCAGGAAGAACCCTCCACCTGCCT GGACCCCAGGCTCGTGGGGAGGTTCCACCTTGGATCCAGGAAGAACCCTCCACCCTGCCT ATGTGCCATGGCCTGCCTCCCCAGTGACCTGCGAAAGTGGAGCATCGAGGTAGGAGGA AACAGCAACCGGGGAGTCCTCGAGCCTGGGGCTGCCCTACCTCTACCCATTCCCCGACCA AACGGCAACCAGGGAGTCCTCGAGCCTGGGGCTGCCCTACCTCTACCCATTCCCCGACCA TGCTTCAGAGGAAGGAAACAAATGAGGGGTGGCAGGGATAAAAAGTCACCTCCATTCTCT 26582 recrircacadaaccaaacaaarcacaccaccaccaccaccaraaaaacrcacccarrcrc TGCCAGCAATGAGTTGGCACTGGCAGAGCTGGAGGAGGAGGAGGCCAAACCCGAGGGCCC 26342 1313 1373 653 713 833 953 1013 1073 1133 1193 1253 1433 1493 593 25682 26042 26522 25742 25802 773 893 25982 26102 26162 26222 26282 26402 26462 셤 셤 g 셤 8 8 ò g 8 8 à 유 ò 임 à g 8 셤 δ 임 셤 ð g ò 셤 ò g ò ò Š 8 유 ð ઠે

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carticonvuleant; antiarthribit; immunosuppressant; immunostimulant; cardiant; thrombolytic; casqulant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antitional antidate antitional antitional antitional antitional antitional antitional antitional associated with an to, or preventing or treating pathological conditions associated with an or or preventing or treating pathological conditions associated with an order and antitional antitional antitional and antitional antitional and antitional and antitional antitiona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 1978-1979; 5507pp; English
30-MAR-2000; 2000US-00540763
                                                                                                                                                                 Shimkets RA, Leach M;
                                                                                (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                              WPI; 2000-602362/57.
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Score 1568.2; DB 3; Length 1666; Pred. No. 0; 0; Mismatches 3; Indels 18; Sequence 1666 BP; 333 A; 529 C; 461 G; 341 T; 0 U; 2 Other; 48.1%; Query Match
Best Local Similarity 98.7
Matches 1598; Conservative

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À	464	CATTAAAGA 52
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! ≿	584	GATGCGTGCCAGCAATGAGTTGGCACTGGCAGGGCTGGAGGAGGAGGAGGCCAAACC
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⋩	644	CGAGGGCCCAGCGAACTCTTCGAAAACCTGCTGGTGCTGAGTCCTGTGTGGGGCACCCCA 703
ą	708	GGCCCAGCGAACTCTTCGAAAACCTGCTGGTGGTGGTCCTGTGTGTG
à		CACGACACCCTCTTCCCTCAGGAGGCCCGTGGGCAGACAGGGGAGCCGGGGGCTTTGCC 763
ą	768	CACGACACCCCTCTTCCCTCAGGAGGCCCGTGGGCAGACAGGGGAGCCGGGGCTTTGCCC 827
≿	764	TGCTGCTGTCTCTCTCGTGTGTGACCCTATTGAGTATCAGTAGCCACTACTCCCCCTGCC 823
ą	828	rdchdcrdrcrcrcrcrdardardcccrarrdadrarcadragccacracrccccrdcc
à	824	1960cc19agagagagactongcnencancracagagagagagagagagagagagagagagagagagag
g Q	888	TGGCCCTGAGAGCGGCTCTGCTCTCTCAAGCAGCCCCTGTCCCCAGCCCGTCCACCC 947
À	884	TGGAGTGGTCTTCTTCAGCCTGTTTCCCCAGCCACAGGCCTGCTACGACCCCCACGATGT 943
q	948	
Ä	944	GCCGCAAGCACTGTCTCACCATCCCGCACCCACCAACAACAGCCAGGCTGGAGTCCAG 1003
qc	1008	GCCGCAAGCACTGTCTCACCATCCCGCACCCACACAGCCAGGGCTGGAGTCCAG 1067
λ	1004	GCCACTTTCAGCTGCTCCTTTCTCCGTGCATGGTGTCTCTTCTCTGCTTTTTTCTCTTC 1063
ąc	1068	GCCACTITCAGCTGCTCCTTTCTCCGTGCATCGTGTCTCTTTTTTTT
λ̈́ζ	1064	CCCCACITCICITICICIGACCCCTCCCCTCCGGIGCGITICGIAICAAAGCICCTCAAA 1123
ą	1128	
à	1124	CCCCGTCCCCCGTGTGTCCTGCTGTGCAGCTCGCTCTTTCCTTCC
q	1188	CCCGTCCCCGTGTGTCCTGTGTGCAGCTCGCTCTTTCCTTCC
à	1184	CAAGGGGATGGACCCAGGCTCGTGGGGGGGGTTCCACCTTGGATCCAGGAAGAACCCTCC 1243
ą	1248	CAAGGGGATGGACCCAGGCTCGTGGGGAGGTTCCACCCTTGGATCCAGGAAGAACCCTCC 1307
à	1244	ACCCIGCCICGIGGGIGGGCCAAAGGCTACAGGGTGCTTCTTCCTCTTCCCCCACCCCCA 1303
ą	1308	ACCCTGCCTCGTGGGTGGGCCAAAGGCTACAGGGTGCTTCCTCCTCTTCCCCCCACCCCCA 1367
à	1304	CTGTCCCTCATGTGCCATGGGCCTGCCTCCCCAGTGACCTGCGAAAGTGGAGCATCGAGG 1363
q C	1368	CTTCCTCATGTGCCATGGGCCTGCCTCCCCAGTGACCTGCGAAAGTGGAGCATCGAGG 1427
à	1364	TAGGAGGAAACAGCAACCGGGGAGTCCTCGAGCCTGGGGCTGCCCTACCTCTACCCATT 1423
ą	1428	
≿	1424	424 CCCGACCAGAGCTTTGCCCTTGCTTGCCTGCCTGCCTCTTTGGGGAACTGAGCTC 1483
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<i>≿</i>	1484	AGAGGCAGGTGCTTCAGAGAAAGAAAATGAGGGGTGGCAGGGATAAAAGTCACCT 1543
qc	1548	GGAGGCAGGTGCTTCAGAGAAAGAAACAAAATGAGGGGTGGCAGGGATAAAAAGTCACCT 1607

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of genes casociated with pharmacogenomics according to one of the sequences of the genes ALDHG (NM 000693), CYPILA (NM 000781), CYPILB1 (NM 000497), CYPIA33 (NM 000776 and NM 017460), DPYD (NM 000781), CYPILB1 (NM 001979), CYPIA33 (NM 000776 and NM 019090, NM 01900, NM 01
1608 CCATTCTCTACCTCCCATGCAGCATGAACACAATTTCTCTCCACCTGGCTCCCAAATTT 1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer.
                                                                                                                                                                                                                                                                       Human, ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour; cytostatic; ALDH6; CYP1181; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
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36.6%; Score 1192.8; DB 6; Length 7924;
Best Local Similarity 75.8%; Pred. No. 2.1e-279;
Matches 1476; Conservative 0; Mismatches 472; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U; 0 Other;
                                                                                                                                                                                                                                  Human chemically pretreated gene sequence #76 strand 1.
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01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG.
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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                antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
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                                                                                                                                                                                                                                                                                                                                                             fragment of chemically modified gene, useful of diseases associated with abnormal cytosine
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    antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
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Pred. No. 2.1e-279;
0; Mismatches 472; Indels
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Matches 1476, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer.
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                                            1621 ATGATTGGGAAAAGGTATGGGAGTAGAAGGAGAATTGGGATTTAGGGTGTAGTTACGTT
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C (NM 002538), TXNRD1 (NM 003330), UGT8 (NM 003360), MRD (NM 004996, NM 019900, NM_019901, NM_019902, NM_019862, NM 019898, NM 019899) and their complementary sequences, or a sequence (S1) chosen from 87 sequences and their complements. The chemical pretreatment is bisulphite treatment to convert cytosines (but not methyl-cytosines) into uracils. The office of the chemical pretricular an oligomer or a peptide nucleic acid (PNA)-oligomer, comprising in each case at least one base sequence having a length of 9 nucleotides which hybridises to or is peptide nucleic acid (PNA)-oligomer, comprising in each case at least one base sequence having a length of 9 nucleotides which hybridises to or is included and their complements, arranged in an array for analysing diseases associated with the methylation state (CpG) and/or detecting SNPs (single nucleotide polymorphisms) of the 87 sequences. The oligomers may also be used as PCR primers. The set of 87 nucleic acids and their complements is useful for diagnosis and therapy of solid tumours and cancer. The present sequence represents one the 87 DNA continuous and cancer. The present sequence represents one the 87 DNA continuous problement directly from WIPO at a continuous or its complement. Note: The sequence data for this patent did continuous into the printed specification, but was obtained in the proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of proposition of propositi
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                                                                                                                               6003
                                          6063
                                                                                                                                                                                                           GCACGCCACCTGCTCCTGAGCCTCCACTATCTCCCTGTGACGGGTGAACTTCGTGTACTG 3137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune system disease; cytosine methylation; antiasthmatic; antianteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiartitic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; articlosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                      TATCTCGAATCCATATATAAATTATAAACAAAATTCATCTATTTTAAACACAAATATTA
                                                                                                                                                                              modified gene, useful with abnormal cytosine
                          ACACGCCACCTACTCCTAAACCTCCACTATCTCCCTATAACGAATAAACTTCGTATACTA
                                                                                       TGTCTCGGGTCCATATATGAATTGTGAGCGGGTTCATCTATTTTAAACACAGATGTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune system associated gene SEQ ID NO: 2112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising fragment of chemically diagnosis and treatment of diseases associated methylation.
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Local Similarity

Best Local Simi Matches 1468;

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TGACCTGCGAAAGTGGAGCATCGAGGTAGGAGGGAAACAGCAACCGGGGAGTCCTCGAGC
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chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastroritestinal; liver disorder; AIDS; ss; acquired immune deficiency syndrome.

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2000US-0249300P.
2000US-0250160P.
2000US-0250391P.
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DB 4; Length 2021;

35.6%; Score 1160.6; DB 4; Length 99.2%; Pred. No. 7.9e-272; tive 0; Mismatches 9; Indels

Query Match
Best Local Similarity 99.2
Matches 1166; Conservative

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182 GATGAAGACCATAGAGGTAGACGCCATCAAAGTGCGGATACAGATCTGGGACACTGCAGG 421

GGATGAGTACGCACCAGGAAGGCGTCCAGAAGATCCTTATTGGGAATAAGGCTGATGAGGA 457

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GCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGATATTTT

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The invention relates to novel isolated polypeptides (1), and

CC polyuclectides (II). (I), (II) and the antibody to (I) are useful for

CC polyuclectides (II). (I), (II) and the antibody to (I) are useful for

CC diagnosing, preventing and treating diseases including immune system

CL disorders (e.g. congenital and acquired immunodeficiencies, autoimmune

CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ

CC transplant rejections and graft versus host disease, infectious diseases

CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and

CC other blood-related disorders (sickle cell anaemia), myeloproliferative

CC disorders, primary haematopoletic disorders, hyperproliferative disorders

CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities

CC Alzheimer's disease, Parkinson's disease), chromosomal disorders (e.g.

CD own syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.

CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),

CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),

CC glomerulonephritis), cardiovascular disorders (e.g. Addison's

CC disease), reproductive system disorders (cirrhosis), as stimulators of

CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of

CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of

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CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of

CC (inflammatory disorders), liver dis
                                                                                                                                                                                                                                                                                                                                                Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.
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08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                            Ruben
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P-PSDB; AAU17136.
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New isolated polypeptide useful for diagnosing and treating immunosuppressive conditions such as autoimmune disease and Parkinson's
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26-JUN-2000; 2000US-0216647P.
07-JUL-2000; 2000US-0216647P.
11-JUL-2000; 2000US-0216647P.
11-JUL-2000; 2000US-021680P.
11-JUL-2000; 2000US-0216290P.
26-JUL-2000; 2000US-0218290P.
26-JUL-2000; 2000US-0229290P.
26-JUL-2000; 2000US-0229261P.
14-AUG-2000; 2000US-022566P.
14-AUG-2000; 2000US-022567P.
14-AUG-2000; 2000US-022567P.
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15-AUG-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229445P.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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                                    GCAGAAACGGCAGGTGGGAAGAGAAGAGCAAGGACAGCTGGCGAAGGAGTATGGCATGGA
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ADB93231;

RESULT 10

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amount of expression of the polypeptide in a biological sample and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the condition based on the presence or amount of expression of the perpetude. The polypeptide is also useful for identifying a binding partner and determining whether the binding partner of feeters an activity of the polypeptide. The polypeptide or the nucleic acid encoding the polypeptide is useful for preventing, treating, or ameliorating a medical condition, which involves administraing the polypeptide or the nucleic acid to a mammalian subject. The nucleic acid is useful for diagnosing a pathological condition or a susceptibility to presence or absence of a mutation in The nucleic acid, and diagnosing a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility or a pathological condition or susceptibility or a pathological condition or susceptibility to a pathological condition or susceptibility or a pathological condition or susceptibility or a pathological condition or susceptibility or a pathological condition and an antibody to the polypeptide are useful as adjuvants to enhance immune responses, and as agents to induce higher a filinity antibodies and increase serum immunoglobulin concentrations. The present sequence represents cDNA encoding a novel human protein. Note:

The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence the necessity and a pathological condition and an electronic form the transfer of the printed sequence the necessity and an electronic format direct from USPTO at
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                                    Gaps
Score 1160.6; DB 9; Length 2021;
Pred. No. 7.9e-272;
0; Mismatches 9; Indels 0;
 Query Match
Best Local Similarity 99.2%;
Matches 1166; Conservative
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Wang D, Liu C, Drmanac RT,
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                                                                                                           The invention relates to an isolated polynuclectide (I) comprising one of 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising daministering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).

(I), (II) and (III) are useful for diagnostic evaluation of disorders.

(I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabettes and allergies. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                       New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.
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Pred. No. 6.5e-233;
0; Mismatches 4; Indels 0;
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                                                                                      Claim 22; SEQ ID NO 74; 284pp + Sequence Listing; English.
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This invention describes novel polypeptide fragments (I) and the polynucleotides (II) that encode them that are highly expressed in a human bladder tunnour and which have cytoateatic activity. (II) are used for recombinant expression of (I) and to isolate complete genes. (I) are directly treat this form of cancer (including expression from gene therapy vectors) or are used in a preparation for cancer treatment. (I) is also used for the generation of specific antibodies. (II) are identified by assembling BSTs (expressed sequence tags) from a particular issue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, and therefore reduces the number of failures associated with the fact that ESTs from
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                                                        Dahl
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                           gene, distorting the estimated frequency of occurrence in a particular tissue. AAZ43260-Z43309 represent expressed sequence tag (BST) fragment isolated from a human bladder tumour CDNA library which encode the procesus represented in AAY66143-Y66198
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                                                                                                                                                                                                                                                                                                                                                                                             2358 AGAACCTCACTTCCTTACTCCTCCAAAAAGAAGTGGGGAAAGAACCATCAAACCTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAACCTCACTTCCTTACTCCTCCAAAAAGAAGTGGGGGAAAGAACCATCAAACCTTTCCT
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different libraries may represent different parts of the same unknown
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                                                                                                                                                                                                                                                             Length 895;
                                                                                                                                                                                         Sequence 895 BP; 249 A; 205 C; 228 G; 213 T; 0 U; 0 Other;
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Matches 879; Conservative
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antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; antiinflammatory; cancer; dimune system disorder; rheumatoid arthitis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlbS; ss;
                                                                                                               Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
                                                                                      cDNA encoding novel signal transduction pathway protein, Seq ID 507
                                                                                                                                                                                                                                  acquired immune deficiency syndrome
                                                                                                                                                                                                                                                                                                                                                            31-JAN-2000; 2000US-0179065P.
04-FEB-2000; 2000US-0180628P.
24-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0186350P.
16-MAR-2000; 2000US-018934P.
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18-APR-2000; 2000US-019013P.

19-MAY. 2000; 2000US-019123P.

28-JUN-2000; 2000US-0219486FP.

28-JUN-2000; 2000US-0215135P.

07-JUL-2000; 2000US-021680P.

11-JUL-2000; 2000US-021680P.

11-JUL-2000; 2000US-021690P.

26-JUL-2000; 2000US-021890P.

26-JUL-2000; 2000US-021819P.

14-AUG-2000; 2000US-022181P.

14-AUG-2000; 2000US-022513P.

14-AUG-2000; 2000US-0225213P.

14-AUG-2000; 2000US-0225214P.

14-AUG-2000; 2000US-0225214P.

14-AUG-2000; 2000US-0225214P.

14-AUG-2000; 2000US-0225214P.

14-AUG-2000; 2000US-0225214P.
         AAS27472 standard; cDNA; 566
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23-AUG-2000;
30-AUG-2000;
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06-SEP-2000;
06-SEP-2000;
                                                             07-NOV-2001
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22-AUG-2000
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                                    AAS27472;
AAS2747
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PR 08-SEP-2000 2000US-021144P

PR 18-SEP-2000 2000US-021340P

PR 14-SEP-2000 2000US-023340P

PR 24-SEP-2000 2000US-023340P

PR 24-SEP-2000 2000US-023340P

PR 25-SEP-2000 2000US-023349P

PR 25-SEP-2000 2000US-023344P

PR 25-SEP-2000 2000US-023444P

PR 25-SEP-2000 2000US-023444P

PR 25-SEP-2000 2000US-023444P

PR 25-SEP-2000 2000US-02444P

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PR 17-NOV-2000; 200008-0249345P.

PR 17-NOV-2000; 200008-0249365P.

PR 17-NOV-2000; 200008-0249365P.

PR 17-NOV-2000; 200008-0249956P.

PR 17-NOV-2000; 200008-024999P.

PR 17-NOV-2000; 200008-024999P.

PR 17-NOV-2000; 200008-024999P.

PR 17-NOV-2000; 200008-024999P.

PR 01-DEC-2000; 200008-024999P.

PR 01-DEC-2000; 200008-025499P.

PR 01-DEC-2000; 200008-02549P.

PR 01-DEC-20009P.

PR 01-DEC-20009P.

PR 01-DEC-20009P.

PR 01-DEC-20009P.

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16.4%; Score 534.2; DB 4; Length 566; 98.9%; Pred. No. 1.2e-119; tive 2; Mismatches 4; Indels 0

Best Local Similarity 98.9 Matches 533; Conservative

Query Match

61 87 TGTGCTGTTCCGGCTGCTGATCGGGGACTCCGGGGTGGGCAAGACCTGCTGTG 121

28 62 88 88 122

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disease.
se; gene; human; autoimmune disease; Parkinson's disease; silicosis; gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia; fimunosuppressive agent; adjuvant; enhance immune response; higher affinity antibody induction; increased serum immunoglobulin concentration.
                                           268 GCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGATATTTT 327
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                                                                                            GGATGAGTACGCACCAGAAGGCGTCCAGAAGATCCTTATTGGGAATAAGGCTGATGAGGA 421
                                                                                                                           422 GCAGAAACGGCAGGTGGGAAGAGAGAGCAGCAGCTGGCGAAGGAGTATGGCATGGA 481
                                                                                                                                                          CTTCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAGTCATTCACGCGTCTGA 540
                                                                                                                                                                   208 GATGAAGACCATAGAGGTAGACGCCATCAAAGTGCGGATACAGATCTGGGACACTGCAGG
GATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAGATCTGGGACACTGCAGG
                                                              GGTCTATGACATTAGCAGCGCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACGT
                                GCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGCCCCAGGGGATATTTTT
                                                                                                                                                                                                                                                              Human cDNA encoding a novel protein #497.
                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0214886P-
2000US-0216647P-
2000US-0217480P-
2000US-0217480P-
2000US-0217496P-
2000US-0218290P-
2000US-022963P-
2000US-022963P-
2000US-022518P-
2000US-0225267P-
2000US-0225267P-
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                                                                                                                                                                                                                 ADB93650 standard; cDNA; 566
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                                                                                                                                                                                                                                                                                                                                            US2002168711-A1
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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The invention relates to an isolated polypeptide. The polypeptide is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, by determining the presence or amount of expression of the polypeptide in a biological sample and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the pathological condition based on the presence or amount of expression of the pathological condition based on the presence or amount of expression of the pathological condition or a susceptibility to a pathological condition which involves contacting the polypeptide with a binding partner and determining whether the binding pathological condition, which involves administering the polypeptide is useful for preventing the polypeptide is useful for preventing the polypeptide is useful for preventing the polypeptide is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, which involves determining the pathological condition in a subject, which involves determining the pathological condition or susceptibility to a pathological condition or based on the presence or absence of the mutation. The polypeptide, the nucleic acid and an antibody to the polypeptide are useful for treating autoimmume disease, Parkinson's disease, silicosis, gastrointestinal disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide, can add and an antibody to the polypeptide are useful for the atline and an antibody are useful as immunosuppressive agents, as adjuvants to enhance immune responses, and as agents to induce higher effinity antibodies and increase serum immunosuppressive or induce data for this patent did not form part of the printed specification but was obtained in electronic format direct from USPTO at sequence the presence or the printed or specification but was obtained in electronic format direct from USPTO at
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05-SEP-2000; 2000US-0229509P.
06-SEP-2000; 2000US-0229513P.
08-SEP-2000; 2000US-023423P.
21-SEP-2000; 2000US-023423P.
21-SEP-2000; 2000US-0234397P.
27-SEP-2000; 2000US-0235837P.
29-SEP-2000; 2000US-023636P.
29-CCT-2000; 2000US-023636P.
20-CCT-2000; 2000US-0237039P.
20-CCT-2000; 2000US-0237039P.
20-CCT-2000; 2000US-0237039P.
20-CCT-2000; 2000US-0237039P.
20-CCT-2000; 2000US-024186P.
20-CCT-2000; 2000US-024186P.
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20-CCT-2000; 2000US-024180P.
217-NOV-2000; 2000US-024180P.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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                                                                 GCCCGCTGCCCGCCCGCAGTTCCCGGCCCCGCTGGCCCCAGTCATGGCGAAGCAGTACGA
                                                                                                                         CCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTAA
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                                                  GCCCGCTGCCCGCCCGCAGTTCCCGGCCCCCGCTGGCCCCAGTCATGGCGAAGCAGTACGA
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Length 566;
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 16.4%; Score 534.2; DB 9; 98.9%; Pred. No. 1.2e-119;
           Pred. No. 1.26
2; Mismatches
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28-MAR-2001; 2001US-0279763P.
29-JUN-2001; 2001US-0302051P.
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                        Conservative
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ses 533; Conserv
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                                                                                                 The invention relates to polynuclectides encoding colon tumour proteins. The polynuclectides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of Colon cancer. Polynuclectide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer. ABK44450-ABK46237 represent. Coding sequences of human colon tumour proteins of the invention. Note: With the exception of SEQ ID No 1 and 2, the sequence data for this patent did not form part of the printed specification but was supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTAGGGAAGTAGGTGATGCCCAGCCCTCAAGTCTGTCTTCAGCCAGGGACTTGAGATTA 2701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for diagnosing, preventing, and treating colon cancer, and as markers for the progression of cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                14.7%; Score 477.4; DB 6; Length 481; 99.4%; Pred. No. 7.7e-106; Live 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 481 BP; 111 A; 113 C; 130 G; 125 T; 0 U; 2 Other;
                                                                Claim 1; SEQ ID NO 303; 147pp; English
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Matches 478; Conservative
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387, App
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Sequence 2, 1
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-671-325-1161	US-09-313-294A-7460	US-08-741-411-6	US-09-016-434-112	US-08-232-463-14	US-09-016-434-813	US-09-016-434-1124	US-08-741-411-4	US-09-075-454-8	US-08-766-551-6	US-09-075-454-11	US-09-620-312D-647	US-09-023-655-7	US-08-741-411-2	US-09-016-434-1159	US-09-621-976-15288	US-09-149-476-54	US-09-493-914-1
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16 Mapplication US/09300958A, 195319 MATION: MCClelland, Michael MCClelland, Michael MCSCLE, John Trenkle, Thomas TENTION: Reduced Complexi FENTION: USing Same VCE: P-FH 3457 ICATION NUMBER: US/09/300 ICATION NUMBER: 60/083,331 3 DATE: 1998-04-27 AATION NUMBER: 60/098,070 3 DATE: 1998-02-04 3 DATE: 1999-02-04 3 DATE: 1999-02-04 30 ID NOS: 85 AATION NUMBER: 60/118,624 AATION NUMBER: 60/18,624 AATION NUM	Scc Pre 0;	555	_ - - - - - - - - - - - - -	999	-8 -8 -8	CTC	AGGC	CATC	GGAG	'AAAG	CTCC
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958A-16 1. Application US/09300958A 1. 6495319 1. TECRNATION: 1. T: MCIELLand, Michael 1. T: TENAKL, Thomas 1. TYENKLE, Thomas 1. TYENKLE, Thomas 1. TYENKLE, THOMER: US/09/300,958A PELING DATE: 1999-04-27 PELICATION NUMBER: 60/098,331 1. LING DATE: 1998-04-27 PELICATION NUMBER: 60/098,700 1. LING DATE: 1998-04-27 PELICATION NUMBER: 60/098,070 1. LING DATE: 1998-02-04 1. LING DATE: 1998-02-04 1. LING DATE: 1998-02-04 1. LING DATE: 1998-02-04 1. LING DATE: 1998-02-04 1. And DATE: 1998-02-04 1. And DATE: 1998-02-04 1. And DATE: 1998-02-04 1. And DATE: 1998-02-04 1. And DATE: 1998-02-04 1. And DATE: 1998-03-04 2. And DATE: 1998-03-04 2. And DATE: 1998-03-04 2. And DATE: 1998-03-04 2. And DATE: 1998-03-04 2. And DATE: 1998-03-04 2. And DATE: 1998-03-04 2. And DATE: 1998-03-04 2. And DATE: 1998-03-04 2. And DATE: 1998-03-04 2. And DATE: 1998-03-04 2. And	Simi 2;			-		-	-				- PG
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US-09-300-958A-16 Sequence 16, App Sequence 16, App Patent No. 6495; GENERAL INFORMA APPLICANT: Mc APPLICANT: Tr TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT PRIOR PELICAT TYPE: DAM OCCUMENT: 730 TYPE: DAM OCCUMENT: 730 TYPE: DAM OCCUMENT: 730 TYPE: DAM OCCUMENT: 730 TYPE: DAM OCCUMENT: 730 TYPE: DAM OCCUMENT: 730 TYPE: DAM OCCUMENT: 730 TYPE: DAM OCCUMENT: 730 TYPE: DAM OCCUMENT: 730	Oue Bes Mat	λ	Db	>	QQ	>	qq	ò	QQ	ò	a Q
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                                      344 aceacercaccacreceaercerrrereacercaacercaccicierreaceaaarcaace 403
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,873
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08824873
Setent No. 5843717
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
TEGISTRATION NUMBER: 35,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
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TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                        57 TACGATGTGCTGTTCCGGCTGCTGATCGGGGACTCCGGGGTGGGCAAGACTTGCCTG
                                                               3; Gaps
al Similarity 59.0%; Pred. No. 3e-31;
305; Conservative 0; Mismatches 209; Indels
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SUSTEM: PEASLES, FOR Windows Version 2.0
SUTREMT APPLICATION DATA:
APPLICATION NUMBER: US/09/198,184
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APPLICANT: duegler, Karl
TITLE OF INVENTION: NOVEL RAB PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STRRET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
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REGISTATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0240 US
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/824,873
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; Sequence 2. Application US/09198184
; Patent No. 6010859
; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
      Best Local Similarity
Matches 305; Conserv
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ecceccecareacccceanareactaccierrraaecrecritrricarresceacrea 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.8%; Score 156; DB 2; Length 925; 56.7%; Pred. No. 3.5e-31; tive 0; Mismatches 220; Indels
              UPERMATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,901
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
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NAME: Bilings, Lucy J.
REGISTATION NUMBER: 36,749
REFERENCE DOCKET NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 925 base pairs
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Diskette
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MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                          Length 1340;
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                                                                                                                                                                                                                                                                                        Score 156.6; DB 3;
Pred. No. 3e-31;
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APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
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Patent No. 5892012
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        4.8%;
                TELEFAX: 415-845-4166
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1340 base pairs
415-855-0555
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 59.09
Matches 305; Conservative
                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                     TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANCNOTO4
CLONE: 738957
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TELEPHONE:
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Gaps . 0 395

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417 CTGGTGGGCAACAAGAGCGACCTCACCACGAGAAGGTGGTGGTGGACAACACCACAGCCAAG 476
                                                                                                                                              477 GAGTTTGCAGACTCTCTGGGCATCCCCTTCTTGGAGACGAGCGCCCAAGAATGCCACCAAT 536
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Pred. No. 8.1e-28;
0; Mismatches 209; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature;
CTHER INFORMATION: Incyte ID No. 6673545 1088524.8
NAME/KEY: unsure;
LOCATION: 2060-2170, 3796, 3799, 3816
OTHER INFORMATION: a, t, c, g, or other
US-09-919-172-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Faris, Mary
APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL Program
                                                                                                                                                                                                                           516 ATTAAAGAGTCATTCACGCGTCTGACAG 543
                                                                                                                                                                                                                                                                                                537 grcgagcaggerrcargaccarggerg 564
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-919-172-49
US-09-919-172-49
; Sequence 49, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
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Best Local Similarity 56.4%;
Matches 270; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 49
LENGTH: 3936
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4.8%; Score 156; DB 4; Length 925;
Best Local Similarity 56.7%; Pred. No. 3.5e-31;
Matches 288; Conservative 0; Mismatches 220; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
STUTARRE: PSESESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,602
                                                                                                                                                                                                                                                                                                    3: Incyte Pharmaceuticals, Inc 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 9F-0367 US
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                             APPLICANT: Lal, Preti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
ALTLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/916,901
                                          Hillman, Jennifer L.
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OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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CLONE: 2514506
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   GENERAL INFORMATION:
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94304
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                                          APPLICANT:
APPLICANT:
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119 GGGTGATGCTTCTTGGGGGANTCGGGCGTCGGCAAAACCTGTTTCCTGATCCAATTCAAG 178
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                                                                                                                                                                                          179 ACGGGGCCTTCCTGTCCGGAACCTTNATAGCCACCGTCGGCATAGACTTCAGGAATAAG 238
                                                                                                                                                                                                                                                                              190 CCATAGAGGTAGACGCCATCAAAGTGCGGATACAGATCTGGGACACTGCAGGGCAGGAGA 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          479 GGGTGATCCGTTCTGAAGATGGAGAGACACTGGCCAGGGAATATGGTGTTCCTTTCATGG 538
239 TGGTGACAGTGGATGGTTCCAGGGTGAAGCTTCAGATCTGGGACACTGCAGGACACAGGAGC 298
                                                                                                                                                                                                                                                                                                                                                                                                                         GATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCCAGGGGATATTTTGGTCTATG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 ACATCACCAACCAGTCCTCTTTTGACAACATCAGGGCCTGGCTCACAGAGATTCATGAGT 418
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IRM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: WORD PERFECT 6.1/MS-DOS 6.2
CURRENT APPLICATION NUMBER: US/09/075,454
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3174 Porter Drive
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REGIGTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0168-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hillman, Jennifer L. APPLICANT: Tang, Y. Tom APPLICANT: Lal, Preeti APPLICANT: Guegler, Karl J. APPLICANT: Guegler, Karl J. APPLICANT: Corley, Nail C. APPLICANT: Patterson, Chandra APPLICANT: Batra, Sajeev APPLICANT: Batra, Sajeev TITLE OF INVENTION: RAS PROTEINS NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,551
FILING DATE: DECEMBER 12, 1996
ATTORNEY/AGENT INFORMATION:
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; Sequence 10, Application US/09075454
; Patent No. 6391580
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ADDRESSEE: INCYTE PR
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APPLICANT: Hillmar
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TOTHER INFORMATION: The n at position 12 represents an unknown.
NAME/KEY: unsure
LOCATION: (14)..(15)
OTHER INFORMATION: The n at positions 14 through 15 represents an OTHER INFORMATION: unknown.
NAME/KEY: unsure
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OTHER INFORMATION: The n at positions 17 through 18 represents an OTHER INFORMATION: unknown.
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LOCATION: (3)
OTHER INFORMATION: The n at position 3 represents an unknown.
NAME/KEY: unsure
LOCATION: (6)..(8)
OTHER INFORMATION: The n at positions 6 through 8 represents an OTHER INFORMATION: unknown.
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OTHER INFORMATION: The n at position 25 represents an unknown.
NAME/KEY: unsure
LOCATION: (726)
OTHER INFORMATION: The n at position 726 represents an unknown.
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OTHER INFORMATION: The n at position 108 represents an unknown.
NAME/KEY: unsure
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COTHER INFORMATION: The n at position 204 represents an unknown.
US-09-255-920A-6
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OTHER INFORMATION: The n at position 22 represents an unknown
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                                                                                                                                                                                          GENERAL INTORNATION:
APPLICANT: Fisher, Joseph
APPLICANT: Lorens, James
APPLICANT: Lorens, James
APPLICANT: Alloy Ying
APPLICANT: Huan, Betty
APPLICANT: Huan, Betty
APPLICANT: Huan, Betty
TITLE OF INVENTION: EXOL and EXO2, EXOCYTOTIC PROTEINS
FILLE REFERENCE: ASS905-1/DJB/RMS
CURRENT APPLICATION NUMBER: US/09/255,920A
CURRENT FILING DATE: 1999-02-23
FRIOR PILING DATE: 1998-02-23
FRIOR PILING DATE: 1998-02-23
FRIOR PILING DATE: 1998-05-23
FRIOR PILING DATE: 1998-05-26
NUMBER: OF SEQ ID NOS: 16
                                                                                                                               Sequence 6, Application US/09255920A
Patent No. 6623980
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LOCATION: (823)
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ORGANISM: Mouse
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SEQ ID NO 6
LENGTH: 842
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234 ACTGCAGGGCAGGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGG 293
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Pred. No. 6.5e-26;
0; Mismatches 193; Indels
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APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL Program
SOFTWARE: 2012
                    FILE REPERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ. ID NOS: 1105
SEQ. ID NO 959
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; Patent No. 6426186
; GENERAL INFORMATION:
Polypeptides
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Best Local Similarity 57.5%;
Matches 265; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , NAME/KEY: CDS
; LOCATION: (124)..(699)
US-09-620-312D-959
TITLE OF INVENTION:
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Pred. No. 5.7e-26;
0; Mismatches 193; Indels
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APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
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Best Local Similarity 57.5%;
Matches 265; Conservative
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Reiyan
                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
TELEFAX: 650-845-4166
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CLONE: 1528559
US-09-075-454-10
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Ma, Yunqing
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NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 646
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 54.6%;
Matches 266; Conservative
PRIOR FILING DATE: 2000-01-21
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                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (156)..(839)
US-09-620-312D-646
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                                                                                                                                      LENGTH: 1069
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4.2%; Score 136.2; DB 4; Length
Best Local Similarity 57.5%; Pred. No. 1.1e-25;
Matches 265; Conservative 0; Mismatches 193; Indels
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TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/552,317
                                   ; FEATURE:
; NAME/KEY: misc_feature
; OTHER INDEMATION: Incyte ID No. 6426186 412477.1CB1
US-09-484-970B-142
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Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Felyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
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Yang, Yonghong
Wang, Jian-Rui
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ORGANISM: Homo sapiens
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229 AGAACTTTGACTACATGTTCAAATTACTCATCATCGGCAATAGCAGTGTGGGGGAAAACAT 288
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Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Joffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
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Length 1069;
Score 133.4; DB 4; Length
Pred. No. 3.5e-25;
0; Mismatches 221; Indels
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SEQ ID NO 828
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         SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
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0; Mismatches 228;
                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1422:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 53.4%;
Matches 261; Conservative
                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: GENBANK
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US-09-016-434-1422
                                                                                                                                       FILING DATE:
CLASSIFICATION:
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RESULT 13 9-09-620-312D-828 ; Sequence 828, Application US/09620312D ; Patent No. 6569662

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Pred. No. 1.4e-22;
0; Mismatches 284;
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TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
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PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
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SOFTWARE: pt_FL_genes Version 1.0
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Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
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Tang, Y. Tom
Liu, Chenghua
Asundi, Vinod
Zhang, Jie
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Wang, Jian-Rui
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Wang, Zhiwei
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ORGANISM: Homo sapiens
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LOCATION: (234)..(875)
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240 GCACCGCTGCTGTCAAGGCTCAGATCTGGGACACAGCTGGCCTGGAGCGGTACCGAGCCA 299
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Pred. No. 7.3e-22;
0; Mismatches 280; Indels
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MEDIUM TYPE: DISKette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/773,423
FILING DATE: Herewith
CLASSIFFCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                            APPLICANT: Goli, Surya K.
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PF-0183 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                5-08-773-423-4
Sequence 4, Application US/08773423
Patent No. 5869291
                                                                                                                                                                                                                                        Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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TYPE: nucleic acid
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702 CGATGGCAG 710
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CLONE: Consensus
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TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                           셤
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                              ACAAGTGCCTGCACCAACCTCAACATTAA---AGAGTCATTCACGCGTCTGACAGAGCTG 548
                                                                            115 TGCTGTGCCGCTTCACCGACAACGAGTTCCACTCGTCGCACATCTCCACCATCGGTGTTG 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 ACTTTAAGATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAGATCTGGGACA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCAGGGCAGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                462 TCATAGTTGTGTATGATGTGACAGATCAGGAGTCCTTCAATAATGTTAAACAGTGGCTGC 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          402 CAGCAGGCCAGGAAAGATTTCGAACAATCACCTCCAGTTATTACAGAGGAGCCCATGGCA 461
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                                                                                                                                   549 GTGCTGCAGGCCCATAGGAAGGAGCTGGAAGGCCTCCGGATGCGTGCCAGCAAT 602
                                                                                                                                                                                    753 TTTGCGAAGGTGTCCAAGCAGAGACAGCATCCGGACCAATGCCATCACT 806
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APPLICANT: Tingley, Debora W.
APPLICANT: Tingley, Debora W.
APPLICANT: Edwards, Carla M.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE FILE REFRENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
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OTHER INFORMATION: Incyte ID No. 6682888 411474.10
NAME/KEY: nusure
LOCATION: 3488-3788
OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/09566921
Patent No. 6682888
GENERAL INFORMATION:
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Best Local Similarity 53.2
Matches 260; Conservative
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ORGANISM: Homo sapiens
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SEQ ID NO 7
LENGTH: 8137
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                                                                                                                360 ACCAGACCTATGCTGGTGGAGGGGATGTGAGGGGCTCTATGACCATGCTGAGGCA 419
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Search completed: March 21, 2004, 02:20:55 Job time : 231 secs

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Sequence 2, Appli
Sequence 2111, Ap
Sequence 151, App
Sequence 152, App
Sequence 152, Appl
Sequence 74, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 20, Appl
Sequence 30, Appl
Sequence 30, Appl
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Sequence 30, Appl
Sequence 31, Appl
Sequence 31, Appl
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11124.786 Million cell updates/sec
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                                                                                                           March 21, 2004, 02:05:45; Search time 1083 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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16 US-10-257-166-152

16 US-10-257-166-152

17 US-10-267-166-152

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Sequence 26, Appl. Sequence 1910, Ap Sequence 1910, Ap Sequence 1910, Ap Sequence 1910, Ap Sequence 204, Appl Sequence 879, Appl Sequence 886, Appl Sequence 886, Appl Sequence 191, Appl Sequence 211, Appl Sequence 211, Appl Sequence 2124, A Sequence 2124, A Sequence 2124, A Sequence 816, Appl Sequence 2124, A Sequence 2124, A Sequence 816, Appl Sequence 2124, A Sequence 816, Appl Sequence 2124, A Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 2124, A Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, Appl Sequence 816, 
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Patent No. US20020146758A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT YE, Jane et al.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO01188
CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12529,
Sequence 58679,
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Sequence 24435,
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2 US-10-085-783A-56703

5 US-10-425-114-2435

2 US-10-424-599-58679
                                    US-09-964-824A-26
US-09-918-995-20848
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US-09-84-257-7
US-09-84-975-885
US-09-834-975-894
US-09-834-975-896
US-09-817-1886-32
US-09-925-300-631
4 US-10-084-817-256
US-09-925-302-91
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100.0%; Pred. No. 0;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 3257; Conservative
TYPE: DNA
ORGANISM: Human
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1321 TGGGCCTGCCTCCCGGTGACCTGCGAAAGTGGAGGATCGAGGTAGGAGGGAAACAGCAA 1380	1501 AGAAGGAAACAAAATGAGGGGTGGCAGGATAAAAAGTCACCTCCTTCTTACCTCCCA 1560	GCACTCCACAAAGGGGAGCATTTGGAAATGAAGGACTAGCTCCTATGTATCAGGTTAAGA 17	186 192 192 198 198		222 222 222 228 228	2281 CAGCCAAACAAAGAACTGGGTGTTGAGTATTCATCAACTAAGAACCAAAATCCAGGGCA 2340
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181 AGATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAGATCTGGGACACTGCGG 240 241 GGCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGGGGCCCAGGGGATATTT 300		541 CAGAGCTGCTGCTGCAGGCCCATAGGAAGCTGGAAGGCCTCCGGATGCCTGCC	CTCAGAGGCCCGTGGGCAGACAGGGGAGCCGGGGCTTTTGCCCTGCTGCTGTCTGT	GCCTGTTTCCCCAGCCACAGCCTGCTACGACCCCACGATGCCGCAAGCACTGTCTC [TEACCCCTCCCTCCGGTGCGTTTCTCTCTCTCTCTCTCCCCCC	CTGGTGTGTGTGCAGGTTGCAGGAGGAGGAGGAGGCCTCCAGCCTGGGGGTG CTGGTGGGGAGGTTCCACCCTTGGATCCAGGAGAAACCTCCACCCTGCGTGGGTG CTGGTGGGGAGGTTCCACCTTGGATCCAGGAAGAACCTCCACCTGCCTG

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Pred. No. 0;
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NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 3
LENGTH: 28770
                                                                                                                                                                                                                          Query Match 82.8%;
Best Local Similarity 98.8%;
Matches 2717; Conservative 0
                                                                                                           ; TYPE: DNA
; ORGANISM: Human
US-09-817-198A-3
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Patent No. US20020146758A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE ITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO01188
CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT FILING DATE: 2001-03-27
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Publication No. US20030143606A1
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APPLICANT: PIEPENBROCK, Christian
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FILE OF INVENTION: Cytosine methylation
FILE REPERBROCE: 5013.1014
CURRENT FILING DATE: 2002-12-16
PRIOR PELLING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
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ORGANISM: Artificial Sequence FEATURE: ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) -10-311-455-2111 36.6%; Score 1192.8; DB 14; Length 7924; Best Local Similarity 75.8%; Pred. No. 0; Matches 1476; Conservative 0; Mismatches 472; Indels 0; Gaps 0; 1276 GGTGCTTCTTCCCTCCCCCCCCTCTGTGCCATGGGCCTGCCT	1 GGIGITTITITITITITITITITITITITITITITITIT	121 GTTTGGGTTGTTTTTTTTTTTTTTGATTAGAGTTTTTGTTTTGTTTGGTTGT 180 1456 CCGCCTGCCTCTTTGGGGAACTGAGCTCAGGGGGGGGGG	241 GÁGGGGTGGTÁGGÁTÁAÁAGTTÁTTTTÁTTTTTTTTTTT	GGGTAAGGAGTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1756 CCAGGGAGTTTGCACAGCAGAGGGAATCTAGCAACAGCAGGCCTCCTAGGCCC	1876 CTAGCCTTCAGCAACCAAGGTTCTCCTGGGACCCAAAGTTTATGGGAGAAGGGCAAAGAC 1935	1996 TITAAGACAAAGGGCTGATCTTGCCCTCTGACATAGGCTTGAGGGTTTGCCAACC 2055	GTTTCTTAACCCCATATGGCCCAAGAGTAGCTGGTAGGAGGCCCTTTAAAGACGGAACA

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: DIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Method and Nucleic Acids for Analysing the
TITLE OF INVENTION: Method and Nucleic Acids for Analysing the
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TITLE OF INVENTION: Method and Nucleic Acids for Analysing the
CURRENT APPLICATION NUMBER: US/10/257,166
CURRENT APPLICATION NUMBER: CONTAIN APPLICATION NUMBER: PCT/EP01/07470
DE 10032529.7
DE 10043826.1
PRIOR FILING DATE: 2001-06-29
2000-06-09
2000-06-00
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Best Local Similarity 75.8%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches 472; Indels
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ORGANISM: Artificial Sequence
FEATURE:
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                              TITCICICCTAGCCCCCTCAGGAAGAAGACTATATITGIACTGTACCCTAGGGGTTCT
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
(MS-10-257-166-152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 35.6%; Score 1160.8; DB 16; Lengt Best Local Similarity 74.1%; Pred. No. 2.4e-309; Matches 1468; Conservative 0; Mismatches 512; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 152, Application US/10257166
Publication No. US20040023230A1
GENERAL INFORMATION:
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By Length 2021; Score 1160.6; DB 9; Length 2021; st Local Similarity 99.2%; Pred. No. 1.2e-309; Ches 1166; Conservative 0; Mismatches 9; Indels 0;
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Qy 482 CTTCTATGAAACAAGTGCCTGCACCTCAACATTAAAGAGTCATTCACGCGTCTGAC 541 Db 518 CTTCTATGAAACAAGTGCCTGCACCTCAACATTAAAGAGTCATTCACGCGTCTGAC 577 Qy 542 AGAGCTGGTGCTGCAGGCCCATAGGAAGGAGCTGGAAAGCCTCCGGATGCGTGCCAGCAA 601 Db 578 AGAGCTGGTGCTGCAGGCCCATAGGAAGGAGCTGGAAGGCCTCCGGATGCGTGCCAGCAA 637 Qy 602 TGAGTTGGTGCTGCAGGCCCATAGGAAGGAGGAGGCAAACCCCGAGGATGCGTGCCAGCAA 637 CQy 602 TGAGTTGGCACTGGCAGGAGGTGGAAGGAGGAAACCCCGAGGGCCCAGCGAACTC 661 Db 638 TGAGTTGGCACTGGCAGAGCTGGAAGGAGGAGCAAACCCCGAGGGCCCAGCGAACTC 661 Db 638 TGAGTTGGCACTGGCAGAGCTGGAAGGAGAGAGAGACCCCAAGGGCCCAAGCGCAAACCCCAAGGGCCCAAGCGCAAACCCCAAGAGACCCCAAGAGACCCAAGAGACCCAAGAGACCCAAGAGACCCAAGAGACCCAAGAGACCCAAGAGACCCAAGAGACCCAAGAGACCCAAGAGACCCAAGAGACCCAAGAGACCCAAGAGACCCAAGAGACCCAAGAGACCCAAGAGACCCAAGAGACCCAAGAGACCCAAGACACCCAAGAGACCCAAGACACCCAAGAGACCCAAGAGACCCAAGACACCCAAAACCCCAAAACCCCAAAACCCCAAAACCCAAAA	Qy 662 TTCGAAAACTGCTGGTGCTGAGTCCTGTGGGGCACCCCCACGACACCCTTTCCC 721 Db 698 TTCGAAAACTGCTGGTGCTGTTGGGCACCCCCCCACACGACACCCCTTTCCC 757 Qy 722 TCAGGAGCCGTGGGAGCACACAGGCACCCCCCCCCCCCC	RESULT 9 US-09-817-198A-28 US-09-817-198A-28 Sequence 28, Application US/09817198A Sequence 28, Application US/09817198A Sequence 28, Application US/09817198A Fatent No. US20020146758A1 GENERAL INFORMATION: TITLE OF INVENTION: TITLE	Query Match 18.4%; Score S99; DB 9; Length 601; Best Local Similarity 99.7%; Pred. No. 1e-154; 10.76 Matches 599; Conservative 1; Mismatches 1; Indels 0; Gaps 0; 0, QY 1076 TTTTCTGACCCCTCCCGGTGGTTTCGTATCAAACTCCTCAAACCCGTCCCCG 1135 0 Db 1 TTCTTCAACCCTCCCTCCGGTGCGTTTCGTATCAAACTCCTCAAACCCGTCCCCG 60 0 QY 1136 TGTGTCCTGTGTGCAGCTCTTTCCTTCCTTCCTTCCTAACCTACCAAGGGGATGGA 1195 0 Db 61 TGTGTCCTGTGTGCAGCTCTTTCCTTCCTTCCTTCCTAAGCTATCCAAGGGGATGGA 120 0 QY 1196 CCCAGGTGTGTGAGGTCCTTTTCCTTTCCTTCCTAAGCTATCCAAGGGATGGA 120 0 QY 1197 CCCAGGTGTGTGAGGTTCCACCCTTGGATCCAAGCTATCCAAGGTATGA 120 0 QY 1197 CCCAGGTTGTGAGGAGTTCCACCCTTGGATCCAGGAAGAACCCTCCACCCTGCTTGT 120 0 DD 121 CCCAGGCTGTGGGGGGGTTCCACCCTTGGATCCAGGAAGAACCCTCCACCCTGCTTGT 180 121 CCCAGGCTCGTGGGGGGGTTCCACCCTTGGATCCAGGAAGAACCCTCCACCCTGCCTG
	WACTED A COURT OF SOLE	Query Match 30.7%; Score 1000.2; DB 12; Length 1054; Best Local Similarity 99.6%; Pred. No. 1.8e-265; Matches 1002; Conservative 0; Mismatches 4; Indels 0; Gaps 0; Qy 2 GCCGGCTGCCCGCCGCGGGTTCCCGGCCCGGCTGGCGGGGGAAGCATACGGGAAGCACACGGGAAGCACACGGCGCGCGC	0y 242 GCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGGGATATTTTT 301 Db 278 GCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGGCCCAGGGGATATTTTT 337 Oy 302 GGTCTATGACATTAGCAGCGAGCGCTCTACCAGCACATCATGAAGTGGGTCAGTGACGT 361 Db 338 GGTCTATGACATTAGCAGCGAGCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACGT 397 Qy 362 GGATGAGTACGCACCAGAAGCGCTCCTTATTGGGAATAAGGCTGATGAGGA 421 Db 398 GGATGAGTACGCACCAGAAGAGCTCCAGAAGAATTTGGGAATAAGGCTGATGAGGA 457 Qy 422 GCAGAAACGCAGCTGGGAAGAGAGCAGCAGCAGCAGCAGCAGAGAATTGGGATTGAGGA 457 Cb 458 GCAGAAACGGCAGGGAAGAAGAGACAAGGCAGCAGCAGCA

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Sequence 7830, Application US/10029386

| Sequence 7830, Application US/10029386
| Publication No. US2030194704A1
| GENERAL INFORMATION:
| APPLICANT: Ren., Sharron G. | APPLICANT: Rank, David R. | APPLICANT: Hanzel, David R. | APPLICANT: Hanzel, David K. | APPLICANT: Hanzel, David K. | APPLICANT: Hanzel, David K. | APPLICANT: Hanzel, David K. | APPLICANT: Hanzel, David K. | APPLICANT: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI | TITLE OF INVENTION: HUMAN GENOME-DERIVED TWO ANALYSIS TWO | FILE REPERENCE: ACONTACT SOUTH OF STOLE OF SEQ ID NOS: 34288 | SOFTWARE: Annomax Sequence Listing Engine vere. 1.1 | SEQ ID NO 7830 | LIENGTH: 594 | LIENGTH: 594
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ORGANISM: Homo sapiens
FEATURE:
CTHER INFORMATION: EXPRESSED IN FEATAL LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
OTHER INFORMATION: EXT HUMAN HIT: BE383632.1, EVALUE 5.70e-01
CTHER INFORMATION: SWISSPROT HIT: P35289, EVALUE 3.00e-14
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569; Conservative
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                                                                                                            1316 TGCCATGGGCCTGCCTCCCCAGTGACCTGCGAAAGTGGAGCATCGAGGTAGGAGGGAAAC 1375
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Batent No. US20020146758A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
FILE REFERENCE: CL001188
CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT PILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
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                                      GGGTGGGCCAAAGGCTACAGGGTGCTTCTTCCTCTTCCCCCCACCCCACTGTCCCTCATG
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Pred. No. 1e-154;
1; Mismatches 1; Indels
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US-09-817-198A-29
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LENGTH: 601
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                             241 AAGGAGAATTGGGATTTTAGGGTGCAGCTACGCTCACCCTAAACTTTTGGTGGCCTGGGG
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2922 AAGGAGAATTGGGGATTTTAGGGTGCAGCTACGCTCACCCTAAACTTTTGGTGGCCTGGGG
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; Sequence 507, Application US/09764868
; Patent No. US2002010.
; Patent No. US2002010.
; Patent No. US2002010.
; APPLICANT: Rosen et al.
; TITLE OP INVENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE OP INVENTION: NUCLE: 2001-01-17
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 507
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NAME/KEY: SITE
LOCATION: (484)
OTHER INFORMATION: n equals a,t,g, 0)
NAME/KEY: SITE
LOCATION: (493)
OTHER INFORMATION: n equals a,t,g, 0)
NAME/KEY: SITE
LOCATION: (538)
OTHER INFORMATION: n equals a,t,g, 0)
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Sequence 30, Application US/09817198A

Patent No. US20020146758A1

GENERAL INFORMATION:

APPLICANT: YE, Jane et al.

TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

FILE REPREMENCE: CLOOL188

CURRENT APPLICATION NUMBER: US/09/817,198A

CURRENT PILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PSESSEQ for Windows Version 4.0

SEQ ID NO 30
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                                   146 CCGAGGCCCAGCGAACTCTTCGAAAACCTGGTGCTGAGTCCTGTGTGGGGCACCCC
                                                                                                               CTGCTGCTGTCCTCTCGTGTGATGACCCTATTGAGTATCAGTAGCCACTACTCCCCCTGC
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ORGANISM: Homo sapien
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Best Local Similarity
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APPLICANT: Meagher, Madeleine Joy
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Meagher, Madeleine Joy
TAPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REPRENCE: 210121.547
CURRENT APPLICATION NUMBER: 105/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 303
LENGTH: 481
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14.7%; Score 477.4; DB 9;
Best Local Similarity 99.4%; Pred. No. 3.6e-121;
Matches 478; Conservative 0; Mismatches 3;
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LOCATION: 417, 461

OTHER INFORMATION: n = A,T,C or G

US-09-920-300A-303
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ORGANISM: Homo sapiens
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                                        208 GATGAAGACCATAGAGGTAGACGCCATCAAAGTGCGGATACAGATCTGGGGACACTGCAGG 267
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Batent No. US20020146758A1
GENERAL INFORMATION.
GENERAL INFORMATION.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUTLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001188
CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
  GATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAGATCTGGGACACTGCAGG
                                                                                   GCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGGCCCAGGGGATATTTTT
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Best Local Similarity 99.8
Matches 516; Conservative
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; ORGANISM: Homo sapien
US-09-817-198A-31
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-09-817-198A-31
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LENGTH: 601
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			0 00 0 00 0 00 0 00 0 00 0 00 0 00 0 0	RESULT 1 CNSLT118T	DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE	AUTHORS TITLE JOURNEL REFERENCE AUTHORS TITLE JOURNAL COMMENT
version 5.1.6 - 2004 Compugen Ltd. w model s:29 ; Search time 7314 Seconds (without alignments) 13297.938 Million cell updates/sec	Cccgcagaaaaaaaaaaaaaaaaaaaaaaaaaa3257 Dext 1.0 14931090276 residues					results predicted by chance to have a . to the score of the result being printed, of the total score distribution. SUMMARIES LID Description CNSIT118T BC014511 BMS51913 BMS51913 BMS51913 BMS51913 BMS51913 BMS51913 BMS97021 BX397021
GenCore Copyright (c) 1993 cleic - nucleic search, using su n: Maxch 21, 2004, 04:56	Title: Perfect score: 3257 Sequence: 1 tgcccgctgcccgccgcag Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched: 27513289 segs, 14931090276	eq length: 0 eq length: 20000000 ing: Minimum Match (Maximum Match)	Database : BST:* 1: em_estba:* 2: em_esthum:* 3: em_estilum:* 5: em_estilum:* 6: em_estilum:* 7: em_estil:* 10: gb_est2:* 11: gb_btc:*			the number of than or equal d by analysis by analysis ch Length DB ch

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into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Libra was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawam Pandoh, Anna-Lista Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Teai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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| organism="Homo sapiens" |
| mol type="mkny see" |
| db xref="taxon:9606" |
| clone="IMAGE:4866926" |
| fissue type="Colon, adenocarcinoma" |
| clone lib="NIH MGC_15" |
| lab host="DH10B-R" |
| /ab host="DH10B-R" |
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ζ	1681	GCACTCCACAAAGGGGGACATTTGGAAATGAAGGACTAGCTCCTATGTATCAGGTTAAGA 1740
q _C	1141	GCACTCCACAAAGGGGAGCATTTGGAAATGAAGGACTAGCTCCTATGTATCAGGTTAAGA 1200
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o o	1801	GGGCCTCCTAGGCCCCATCTTCCATTTCTTAGGTAAGAAGAGCATTTCCTCAGACTCCCA 1860
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 1081) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE JOURNAL Unpublished (1999) COMMENT Email: cgapbs-remail.nih.gov Fissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CONNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be the procure of the procure of the procure of the procure of the procupation of through the 1.M.A.G.E. Consortium/LLNL at:	PLATE: LLCM200 row: k column: 18 High quality sequence stop: 662. FEATURES Location/Qualifiers 1. 1081 /mol_type="mRNA" /db_xref="taxon:9606"	/clone="INAGE:5479433" /tisbue_type="astrocytoma grade IV, cell line" /lab host="Hillo" (phage-resistant)" /clone lib="NIH MGC 98" /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adapcor: GGCACGAG(G). Library constructed by Ling Hong	in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologie Note: this is a NIH_MGC Library."	Query Match 29.1%; Score 947.8; DB 12; Length 1081; Best Local Similarity 95.4%; Pred. No. 8.2e-133; Matches 1029; Conservative 0; Mismatches 44; Indels 6; Gaps 5; Qy 1178 GCTATCCAGGATGGATGGACGAGGTTCCACCTTGGATCCAGGAAA 1237	Db 1 GTATCCAGGGATGGACCTGTGGGGGGGGTTCCCCTTGGATCCAGGAAGAA 60 Qy 1238 CCTTCCACCTGCTGGGGGGGCCAAAGGCTACAGGGTGCTTCTTCTTCTTCCCCA 1297 HILLIHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1298 CCCCACTGCCCCATGCCATGGCCTGCTCCCCCAGTGACCTGCTGCGAAAGTGGAGCA 1210 CCCCACTGCCATGCCATGGCCTGCCTCCCCCAGTGACCTGCGAAAGTGGAGCA 121 CCCCCACTGTCCCTCATGGCCTGCCTGCCTCCCCAGTGACCTGCGAAGTGGAGCA	Qy 1358 TCGAGGTAGGAGAAACAGCAACCGGGAGTCCTCGAGCCTGGGGCTGCCCTAACTCTA 1417 Db 181 TCGAGGTAGGAGAAACGGAGAGTCCTCGGGGCTGCCTGCTTACTCTTA 240 Qy 1418 CCCCTACCCGACACTTGCCCTTGCTTGCCCTTTTGGGGAACT 1477	Db 241 CCCATTCCCGACCAGACTTTGCTTGCTTGCTGCCGCTGCCTTTGGGAAACT 300 Qy 1478 GAGCTCAGAGAGACTTCAGAGAACAAAAAAAAAAAAAAA	1538 TCACCTCCATCTCTACCTCCCATGCAGCATGAACAATTTCTCTCCACCTGGCTCCCA	Qy 1598 AATTTAAAGATGTGGACCAAGGGCTGTGGGGACCCAGGGGCCAGGGGCCTGGGGTC 1657
2341 CTCATATGTGAAGGATAAGAACCTCACTTCCTTACTCCTCCAAAAAGAAGAAGAAGAAAGA	1981 ATCACTGGCTAATGAGAAAGGAGACAGCTAACTCTAGGATGAAGCTGTGGCTGGGTGGG	Oy 2641 GCTAGGGAAGTAGCCAACCCCTCAAGTCTTCAGCAGGACTTGAGAAGTT 2700	GGGTGCCATTCATTGTCTTCTCTCCTAGCCCCCTCAGGAAGAACTATATT	Db 2281 TGTACCCTAGGGGTTCTGGAAAGGGAAAACATGGAATTCTATAGACTGTTAGGCC 2340 Qy 2881 CTATCCACAAGGGCCATGACTGGGAAAAGGTATGGGAAAGGAAATTGGGATTTTA 2940 L	2941 GGGTGCAGCTACGCTCACCCTAAACTTTTGGTGGCCTGGGGCATGTCTTGAGGCCCAGACCCAGACCCTTTTGGTGGCCTGGGGCATGTCTTGAGGCCCAGACCAGACCCAGACCCTGGGGCCTGGGGCATGTCTTGAGGCCTGGGCCTGGGCCTGGGCCTGGGCCTGGGCCTGGGCCTGGGCCAGACCAGACAACAAAAAAAA	QY 3001 TGTTAAGCAGGCTCTGGTTACTCGTCACCACCTCCTCTCTTGGG 3000 Db 2461 TGTTAAGCAGGCTCTGCTGTTTACTCGTCACCACCTCTGCACTGCTGTTTAGG 2520 Qy 3061 ACTCCATCCAGGCACGCCACGCTGCTCCTGAGCTCCTCTGTGAGG 3120	Db 2521 ACTCCATCCAGCCCCAGCCACCTCCTCAGACCTCCATATCTCCCTGTGACGG 2580 Qy 3121 GTGAACTTCGTGTACTGTCTCGGGTCCATATATGAATTGTGAGGGTTCATCTATT 3180	Qy 3181 TTAAACACAGATGTTTACAAAATAAAGATTATTTCAAACCACCAAAAAAAA	RESULT 3 BM551913 LOCUS BM551913 LOCUS DEFINITION AGENCOURT 6575472 NIH_MGC_98 Homo sapiens CDNA clone IMAGE:5479433 5', mRNA Sequence.	ACCESSION BM551913 VERSION BM551913.1 GI:18789340 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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cgi-bin/cluster.cgi?seq=CSODI028AG06_DI1486_2&cluster=7307.r.
contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ invitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODI028AG06_DI1486_2.
Location/Qualifiers
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BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7307.r
more information about this cluster, see
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 956)
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/tissue type="PlACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a Not!-Oigo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                                                                                               CCAAATTAAAGATGTGGACC-AGGCCTGTGGGTACTCCAGGGGCAAGGAGAGCCCTGGGG
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                                                                                                                                                        Score 883.4; DB 13; Length 956;
Pred. No. 4e-123;
); Mismatches 9; Indels 5;
                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                            27.1%;
                                                                                                                                                                Query Match 27.1
Best Local Similarity 98.5
Matches 942; Conservative
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1673

1733

420

1793

480

1853

540

600

us-09-817-198c-1.rst

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BX397020 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA colone CSOD1028YM11 5-PRIME, mRNA sequence.
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1 (bases 1 to 915)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                        301 CCAAGGCCTGTGGGTACTCCAGGGCAAGGAGCCCTGGGGTCAGTGACGTCAGGC
                                                                                                                                                                                                                                                                                                                                    2154 GAGGCCCTTTAAAGACGGAACAAGTAATTTACCAGTTCTACTGGGGTTCCTGC-CCACCG
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                                                                                                                                                                  361 CAACCATGCACTCCACAAAGGGGAGCATTTGGAAATGAAGGACTAGCTCCTATGTATCAG
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Genescope - Centre National de Sequencage
Genescope - Centre National de Sequencage
BP 191 91006 EVRY
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7307.rr
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi1seq=cS0D1028AG06 D11486 L&cluster=7307.r.
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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/lab_host="DH10B (phage-resistant)"
/clone_lib="With MGC_40"
/clone_lib="With MGC_40"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: BCoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the birectionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                     957 bp mRNA linear EST 21-AUG-2002
AGENCOURT 10018726 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6482195
5', mRNA Sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM2664 row: m column: 12
High quality sequence stop: 555.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6482195"
                                                                                                                                                                                                                                      BQ937298.1 GI:22352681
                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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/note="lst strand cDNA was primed with a Not1-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Avenue Genoscope sequence ID : CSODI028AG06_D11486_1. Location/Qualifiers
                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                26.0%; Score 847.2; DB 13; Length 915; 98.3%; Pred. No. 1.1e-117;
                                                                                                                                                                                                                                                                                   0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                  Best Local Similarity 98.3
Matches 882; Conservative
     Faraday
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AGENCOURT 8217893 Lupski sympathetic_trunk Homo sapiens cDNA clone
IMAGE:6187941 5', mRNA sequence.
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801 GAAAGAACCATCAAACCTTTTCTNCTGACTTACCAAACCAGG-AAACAGCNAGAGAGGGT 859
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(Dases 1 to 908)

NIH-MGC http://mgc.nci.nih.gov/
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                                                                                                                                      860 GGCTCAGGACTTAGGGACAGGGTATAGCTNANATGGT-GAAAGCAAAGGAGGAGCAGG
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ilarity 97.6%; Pred. No. 1.3e-116;
Conservative 0; Mismatches 19; 1
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Location/Qualifiers
1. 908
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/mol type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:6187941"
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/tissue_type="PLACENTA COT 25-NORMALIZED"
./clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
//note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7307.r For more information about this cluster, see http://www.genoscope.rns.fr/
cgi-bin/cluster.cgi?seq=CSOBAA015ZB10 CS01419_1&cluster=7307.r.
Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSOBAA015ZB10_CS01419_1.
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ilarity 97.9%; Pred. No. 2.9e-116;
Conservative 0; Mismatches 18;
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/db_xref="taxon:9606"
/clone="CS0DI028YM11"
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1. (bases 1 to 918)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                                                                 GTGGGTGGGCCAAAGGCTACAGGGTGCTTCTTCCTCTTCCCCCCACCCCCCACTGTCCTCA
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
En (bases 1 to 929)
I (bases 1 to 929)
I (w.B. Gruber.C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 BYRY cedex - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7307.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAF024ZB10_AF02283_2&cluster=7307.r.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2760 AGGGTGCCATTCATTGTCTTTCTCTTAGCCCCCTCAGGAAAGAAGAAGAATATTTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 GAGTTGCTTCCTTGAAGATGGGACTCCTTGGGTATCAAGACCTATGCCACATGACACTGG
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                                                                                             241 AACCATCAAACCTTTCCTCCTGACTTACCAAACAGGAAAACAGCAGGAGAGAGGGTGCTC
                                                                                                                                     2460 AGGACTTAGGGACAGGGTATAGCTTAGATGGTGGAAAGCAAAGGAGGAGCAGGAAGTTGTA
                                                                                                                                                         2520 AATCACTGGCTAATGAGAAAAGGAGACAGCTAACTCTAGGATGAAGCTGTGACTAGGCTG
                                                                                                                                                                                                                                    2580 GAGTTGCTTCGAAGATGGGACTCCTTGGGTATCAAGACCTATGCCACATCACACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                        481 GGCTAGGGAAGTAGGTGATGCCAGCCCTCAAGTCTGTCTTCAGCCAGGGACTTGAGAAGT
                                                             2400 AACCATCAAACCTTTCCTCCTGACTTACCAAACCAGGAAAACAGCAGGAGGGGTGGCTC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 901)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Rish quality sequence stop: 606.

High quality sequence stop: 606.
                                                                                                                                                                                                                                                                              AGENCOURT 7594485 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6061422 S', mRNA Sequence.
BQ220195.1 GI:20401595
EST.
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                               / organism="Homo sapiens"
/mol type="mRNA"
/db Xref="taxon:9606"
/clone="ImAG8:605422"
/tissue_type="melanotic melanoma"
/tab_bost="DH10B (phage-resistant)"
/clone_lib="NHH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not!;
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not!;
/average insert size 2 kb. Library constructed by Life
Technologies."
                                                 160 TCTTTCCTTCCTTCCTAAGCTATCCAAGGGATGGACCCCAGGCTCGTGGGGGGTTCCAC 1215
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Pred. No. 3.5e-112;
0; Mismatches 9; Indels 2;
                                                                                                                                                                                   1220 CCTTGGATCCAGGAAGAACCCTCCAC 1245
                                                                                                                                                                                                           CCTTGGATCCAGGAAGAACCTGCCC 917
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98.7%;
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Best Local Similarity 98.73
Matches 838; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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ilarity 93.7%;
Conservative
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Best Local Si
Matches 868
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                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="taxon:9606"
/clone="CSODIOSYMAIN"
/tissus_type="Flacenta COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EOOR V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            546
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                http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAF024ZBIO_AF02283_;
Location/Qualifiers
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8
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Pred. No. 9.2e-112;
0; Mismatches 26; Indels 8;
: Feng Liang Email : fliang@lifetech.com URL
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Matches 899; Conservative
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/dione="INAGE:SOLST13"
/tissue_type="small cell carcinoma"
/tissue_type="small cell carcinoma"
/tissue_type="small cell carcinoma"
/tissue_type="maging"
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/note="organ: lung; Vector: pOTB7; Site_1: Xho1; Site_2: EcoR1; cDNA made by oligo-dr priming. Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAA-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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BI118034
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 924)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DcTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1825 row: b column: 02
High quality sequence stop: 893.
Location/Qualifiers
                                        GTGTGCAGCTCGCTCTTTC--TTCCTTCCAAGCTATCCAAGGGGATGGACCCAGGCTCGG
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National Institutes of Health, Mammalian Gene Collection (MGC)
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0; Mismatches 54;
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2147 CTCGTAGGAGGCCCTTTAAAGACGGAACAAGTAATTTTACCAGTTCTACTGGGGTTCCTGC 2206
Fissue Procurement: ATCC
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TGGGTACTCCAGGGCAAGGAGAGACCCTGGGGTCAGTGACACTGTCAGGCCAACCATGCA 181
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1046)

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                                                 crccacaaaggggagcarrrggaaargaaggacragcrccrargrarcaggrraagagca
                                                                          AGGGAGGTGGCCAGGGACAGCTTTGCACAGCAGAGGGAATGTAGCAACAGCAGGG
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MG clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Blate: LLGN2042 row: h column: 06
High quality sequence stop: 570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 24.5%; Score 799.2; DB 13; Length 1046; Best Local Similarity 96.9%; Pred. No. 1.7e-110; Matches 847; Conservative 0; Mismatches 23; Indels 4;
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3096 AGCCTCCACTATCTCCCTGTGACGGGTGAACTTCGTGTACTGTGTCTCGGGTCCATATAT 3155
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                                                                              98 AGCAAAGGAGAGGAGGAAGTTGTAAATCACTGGCTAATGAGAAAAGGAGACAGCTAAACTC
                                                                                                                                                                                     TAGGATGAAGCTGTAGACTGGAGTTGCTTCCTTGAAGATGGGACTCCTTGGGTATC
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38 GGAAACAGCAGGAGAGGGTGGCTCAGGACTTAGGGACAGGGTATAGCTTAGATGGTGGAA
                                                                                                                                                          TAGGATGAAGCTGTGACTAGGCTGGAGTTGCTTCCTTGAAGATGGGACTCCTTGGGTATC
                                                                                                                                                                                                                                                                AAGACCTATGCCACATCACACTGGGGCTAGGGAAGTAGGTGATGCCAGCCCTCAAGTCTG
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//Lisbue_Lype="teratocarcinoma, cell line"
//Lib host="DHIOB (phage-resistant)"
//Lib host="DHIOB (phage-resistant)"
//Lib host="Organ: Oracy; Vector: pOTB7; Site_1: EcoRI; Site_2:
//Lib host="Organ: Oracy; Vector: poTB7; Site_1: EcoRI; Site_2:
//Lib host="Organ: Oracy; Vector: poTB7; Site_1: EcoRI; Site_2:
//Lib host="Organ: Oracy; Vector: poTB7; Site_1: EcoRI; Site_2:
//Lib host="Organ: Oracy; Vector: poTB7; Vector: Disputable oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potential oracy; Vector: Potent
                                                                              2266
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                                                                                                                                                                                     2267 GCACTGCGTGCCTGCAGCCAAAACAAAGAACTGGGTGTTGAGTATTCATCAACTAAGAAC 2326
                                                                                                                                                                                                                                                                                         2327 CAAAATCCAGGGCACTCATATGT-GAAGGATAAGAACC--TCACTTCCTTACTCCTCCAA 2383
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 840)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov forw: f column: 22
High quality sequence start: 32
High quality sequence stop: 727.
Location/Qualifiers
CTCCTATGAGGCCCTTTAAAGACGGAACAAGGAATTTACCAGTTCTACTGGGGGTCCTGC
                                                                                                            CCACCGTCCCCAAGGTGGGCGAGGCCTATGAAGAGGTCATTCTTAAGCCACACACTTAGCT
                                                                                                                                                                                                                   GCACTGCGTGGCTGCCGAAAACAAAGAACTGGGGGTGGAGGATTCATCAGCTAAGAAC
                                                                              CCACCGTCCCAAGGTGGGCGAGGCCTAGGAAGAGGGTCATTCTTAAGCCACACATTAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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JOURNAL
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AGENCOURT 10440477 NIH MGC_109 Homo sapiens cDNA clone IMAGE:6598564 5', mRNA sequence.
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1 (bases 1 to 820)

NIH-WGC http://mgc.ndi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (WGC)
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
                                                                                                      BU849866.1 GI:24034829
                                                                                                                                                   sapiens (human)
sapiens
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AUTHORS
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2436 GAAAACAGCAGGAGAGAGGGTGGCTCAGGACTTAGGGACAGGGTATAGCTTAGATGGTGGAA 2495

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/organism="Homo sapiens"

/mol_type="mRNA"

/mol_type="mRNA"

/db_xref="hazon:9606"

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/tlone lib="NNH MGC 109"

/clone lib="NNH MGC 109"

/clone lib="NNH MGC 109"

/clone lib="NNH MGC 109"

/khof; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/KhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript I RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 16-SEP-2002
                                                                                                                                                                                                                             661 GAGCCTCCACTATCTCCCTGTGACGGGTGAACTTCGTGTACTGTGTCTCGGGTTCCATATA 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ATGTGGACCAAGGCCTGTGGGTACTCCAGGGCAAGGAGAGCCCTGGGGTCAGTGACACT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                            601 ACCACCTCTGCACCTGCTGTCTTGAGACTCCATCCAGCCCCAGGCACGCCACCTGCTCCT
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                                                                                                                                                                                                   TGAATTGTGAGCAGGGTTCATCTATTTAAACACAGATGTTTACAAAATAAAGATTATTT
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can though the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2796 row: i column: 19
High quality sequence stop: 679.
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AGENCOURT 10253405 NIH MGC 109 Homo sapiens cDNA clone
IMAGE:6585115 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                             3215 CAAACCACCAAAAAAAAAAAAAA 3239
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1 (bases 1 to 863)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"

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/mol_type="mxxx"
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/tissue_type="teratocarcinoma, cell line"
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/clone lib="WIH MGD (phage-resistant)"
/clone lib="WIH MGD (l09"
/note="Organ: ovary; Vector: pOTB7; Site_1: EcoR1; Site_2:
Xho1; cDNA made by oligo-dT priming. Directionally cloned
into EcoR1/Xho1 sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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                       cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequenoring by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2831 row: j column: 04
High quality sequence stop: 668.
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GTCAGGCCAACCATGCACTCCACAAAGGGGAGCATTTGGAAATGAAGGACTAGCTCCTAT 1726	TCCTCAGACTCCCAGGCGGAGGACTGAGCCTTCAGCAACCAAGGTTCTCCTGGGA TCCTCAGACTCCCCAGGCGGAGGACTGAGCCTTCAGCAACCAAGGTTCTCCTGGGA TCCTCAGACTTCCCAGGCGGAGGACTGAGCCTTCAGGCAACCAAGGTTCTCCTGGGA CCCAAAGTTTATGGGAGAAGGCCAAAGACTTCATGGGAAGAGAAGGCCCTGGGT CCCAAAGTTTATGGGAAAGGCCAAAGACTTCATGGGAAGAGAAGGCCCTGGGT CCCAAAGTTTATGGGAAAGGCCAAAGACTTCATGGGAAGAGAAGGCCCTGGGT AGAAACGCTTGGTGCTGTTTTTGGCCTTTTAGACAAAGCGCCTTTACAGAAAGGCCCTTACCTTACAAAGCCTTTACCCCTCTAC AGAAACGCTTGGTGCTGTTTTTTGGCCTTTTAAGACAAAGCGCTCATCTTGCCCTCTAC ACAAACGCTTGGTGCTGTTCTCTTTTTAAGACAAAGCGCTCATCTTGCCCTCTAC	CTCCTGATAGGCTTGAGGGTTTGCCAACCACTGTGGCTACAGGTGGAGGGAAGAGGAC 2086	CCACCGTCCCAAGGTGGGCGAGGCCTAGGAAGGGTCATTCTTAAGCCACACATTAGCT
121 121 1727 181 1787 241	1847 301 1907 361 1967 421	2027 481 2087 541 2147 601	2207 661 2267 721 2327 781 2384 841
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Search completed: March 21, 2004, 11:01:47 Job time : 7335 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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March 15, 2004, 11:08:42 ; Search time 60 Seconds (without alignments) 998.335 Million cell updates/sec Run on:

US-09-817-198C-2

score: Title: Perfect

1 MAKQYDVLFRLLLIGDSGVG......LEEBEGKPEGPANSSKTCWC 212 Sequence:

1586107 segs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

1586107

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_29Jan04:* 1: genesedp1980s:* geneseqp1980s:* geneseqp1990s:* geneseqp2001s:* geneseqp2004s:* geneseqp2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Abp62882 Human pol	Aae29096 Human Ras	Aaul7136 Novel sig	Adb93844 Human nov	Aab41604 Human ORF	Ade58127 Rat Prote	Aau17555 Novel sig	Adb94263 Human nov	Abb70670 Drosophi	Ade58121 Human Pro	Abbi1916 Human rak	Abp41333 Human ova	Ade83429 Human Pro	Ade58125 Human Pro	Aab58196 Lung canc	Aab09979 Human Rab	Aab19165 Amino aci	Aab95340 Human pro	Aab56993 Human pro	Abg07266 Novel hum	Abb71647 Drosophi	Aag67154 Amino aci	Aab92628 Human pro	Abp65204 Hypoxia-r	
SOLUTION TO S	ID	ABP62882	AAE29096	AAU17136	ADB93844	AAB41604	ADE58127	AAU17555	ADB94263	ABB70670	ADE58121	ABB11916	ABP41333	ADE83429	ADE58125	AAB58196	AAB09979	AAB19165	AAB95340	AAB56993	ABG07266	ABB71647	AAG67154	AAB92628	ABP65204	נסססססמיני
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d	Query Match	100.0	100.0	100.0	100.0	98.8	97.5	75.3	75.3	49.5	49.3	49.3	48.9	48.1	48.1	48.1	48.0	48.0	48.0	48.0	47.9	47.8	47.8	47.8	47.8	,
	Score	1105	1105	1105	1105	1092	1077	832	832	546.5	545	545	540	532	532	532	530.5	530.5	530.5	530.5	529.5	528.5	528.5	528.5	528.5	
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	ADJ25583 Aspergill Aag53945 Arabidops Aag08688 Arabidops Aag53944 Arabidops	Aag08687 Arabidops Aao19956 C elegans Aag35215 Zea mays	Aa026373 Ras-like Aag19220 Arabidops Aag08006 Arabidops Abg23365 Novel hum	Arabid Arabid Novel	Aao15989 Human Ras Ada09336 Human GTP Aay00919 Human Rab
AAB09980 AAB09981 ABJ26542	ABJ25583 AAG53945 AAG08688 AAG53944	AAG08687 AAO19956 AAG35215	AAO26373 AAG19220 AAG08006 ABG23365	AAG47826 AAG47825 ABG23366	AAO15989 ADA09336 AAY00919
199 3 199 3 206 6	206 6 216 3 216 3 253 3	254 3 201 6 215 3	190 6 218 3 216 3 209 4	224 3 234 3 335 4	256 6 256 7 201 2
47.3	47.3 47.0 47.0	47.0 46.5 6.5	4 4 4 4 4 6 .3 4 4 5 . 2 6 . 3 8 . 3	45 65.3 6.6.6.	4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
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26 27 28	33309	334	33 33 39 39	4 4 4 2 4 2	4 4 4 6 4 4 5 5

ALIGNMENTS

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antiparkinsonian; immunostimulant; cytostatic; immunosuppressive; antidiabetic; antiallergic; gene therapy; wound healing; tissue repair; burn; central nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; immune disorder; autoimmune disorder; multiple sclerosis; diabetes; allergy.
                                                                                     Human; vulnerary; dermatological; neuroprotective; nootropic; cancer;
                ABP62882 standard; protein; 212 AA
                                                                    Human polypeptide SEQ ID NO 319.
                                                  (first entry)
                                                  14-OCT-2002
                                  ABP62882;
RESULT 1
          ABP6288
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Homo sapiens.

WO200218424-A2.

07-MAR-2002.

31-AUG-2001; 2001WO-US027093.

01-SEP-2000; 2000US-00654935.

(HYSE-) HYSEQ INC.

Wang J; Zhang J, Ren F, Zhar Wehrman T; Zhou P, Xue AJ, u C, Drmanac RT, Asundi V, Zno Tang YT, Zhao QA,

WPI; 2002-583321/62.

N-PSDB; ABQ93361.

New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.

Claim 20; SEQ ID NO 319; 284pp + Sequence Listing; English.

The invention relates to an isolated polynucleotide (I) comprising one of 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising administering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II). (I), (II) and (III) are useful for diagnostic evaluation of disorders (I) is useful for gene therapy of diseases and (II) can be used for

/note= "Protein kinase C phosphorylation site"

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therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                     INDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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ce= "Casein kinase II phosphorylation site"
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/note= "Protein kinase C phosphorylation site"
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                                                                                                                                                                            Length 212;
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note= "ATP/GTP binding site motif A"
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100.0%; Pred. No. 1.4e-108;
tive 0; Mismatches 0;
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/note= "N-glycosylation site"
206. .208
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es 212; Conserv
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The invention relates to human Ras-like protein and its corresponding nucleic acid. The Ras-like protein and DNA is useful in the development of nucleic acid. The Ras-like protein and DNA is useful in the development of human therapeutics and diagnostic compositions. They are useful in the diagnosis, prevention and disorders associated with cell proliferation and apoptosis, e.g. AIDS and other inflectious or genetic immunodeficiencies, neurodegenerative disease e.g. Alzheimer's disease, Parkinson's disease, wasting diseases e.g. cachexia, circhaemic injuries e.g. myocardial infarction, stroke or repertusion injury, toxin-induced diseases such as alcohol-induced liver damage or cirrhosis, osteoporosis or cancer. They are also used to treat disorders associated with inflammation including allergies, atopic dermatitis, atherosclerosis, asthma, anaemia, Crohn's disease, diabetes mellitus, casociated with inflammation including allergies, disease, glomentulomephritis, gout, irritable benel syndrome, clupus erythematosus, multiple sclerosis, sosteoarthritis, pandreme, untiple sclerosis, osteoarthritis, pandreme, cuestis, trauma, or viral, bacterial, fungal, parasitic, protozoal or halminthic infections. The antibodies of the invention are useful in the pharmacognomic analysis or for tissue typing. The transgenic animals are cueful for studying the function of a Ras-like protein is used in drug screening assays and its activity. Ras-like protein is used in care therapy. The present cycle sequence is human Ras-like protein
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Best Local Similarity 100.0%; Pred. No. 1.4e-108;
Matches 212; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                          Gan W, Ye J, Di Francesco V,
                                                                                                                             27-MAR-2002; 2002WO-US009328
                                                                                                                                                                       27-MAR-2001; 2001US-00817198
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08-SEP-2000; 2000US-0232081P.
12-SEP-2000; 2000US-023293P.
14-SEP-2000; 2000US-0232398P.
14-SEP-2000; 2000US-0232399P.
14-SEP-2000; 2000US-0232399P.
14-SEP-2000; 2000US-0232400P.
14-SEP-2000; 2000US-0233649.
14-SEP-2000; 2000US-0233663P.
14-SEP-2000; 2000US-0233664P.
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2000US-0234274P.
2000US-0234997P.
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2000US-0249210P.
2000US-0249211P.
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02-0CT-2000;
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13-0CT-2000;
13-0CT-2000;
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17-NOV-2000;
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  08-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sofice cell anaemia; hyperproliferative disorder; Gancher's disease; neurodegenerative disorder; Alzheimer's disease; parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlDS; acquired immune deficiency syndrome.
                                                                                                        Novel signal transduction pathway protein, Seq ID 701
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2000US - 0218290P

2000US - 0220964P

2000US - 0224518P

2000US - 0224518P

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2000US - 0225266P

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2000US-0189874P.
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                                                              07-NOV-2001 (first entry)
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08-SEP-2000;
08-SEP-2000;
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16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-JUN-2000;
28-JUN-2000;
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                  AAU17136;
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Homo sapiens.
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                                                            ADB93844;
            ADB93844
                                                            the invertion traters to mover beingboth to (1) and the antibody to (1) are useful for diagnostics, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune closorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. congenital archiritis), inflammatory conditions, organ transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin annormalities and cother blood-related disorders (sickle cell anaemia), mysloproliferative disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. daucher's disease and cancer), neurodegentrative disorders (e.g. Alzheimer's disease and cancer), neurodegentrative disorders (e.g. Alzheimer's disease). Chromosomal abnormalities (c.g. gomerulonephitis), cardiovascular disorders (e.g. arthythmia), respiratory disorders, cardiovascular disorders (e.g. Arthythmia), captublish cell proliferation, endocrine disorders (e.g. Addison's disease), reproductive system disorders (cirthosis), as stimulators of (inflammatory disorders), liver disorders (cirthosis), as stimulators of B-call responsiveness to pathogens, activators of T-cells, to induce thigher affinity antibodies, and as a means to induce (unour proliferation of npathway protein, amino acid ANUT7683 represent novel signal transduction pathway protein, amino acid sequences of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel isolated polypeptides (I), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RMRASNELALAELEEEGKPEGPANSSKTCWC 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 701; 880pp; English.
                                                                                                                                                                                                                                                                                          Ruben SM;
                                                                                  2000US-0256719P.
                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
                2000US-0250160P
                                                                                                                    2000US-0251856P
                                                                                                                                                                                      2000US-0251990P
                                                                                                                                                                                                                        05-JAN-2001; 2001US-0259678P
2000US-0249300P
                              2000US-0250391P
                                                                                                                                    2000US-0251868P
                                                                                                                                                                                                       2000US-0254097P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 212; Conservative
                                                                                                                                                                                                                                                                                          Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                            WPI; 2001-465460/50.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS27053.
                                                05-DEC-2000;
05-DEC-2000;
                                                                                   05-DEC-2000;
                                                                                                                                                                    08-DEC-2000;
                                                                                                                                                                                                      11-DEC-2000;
                                                                                                                                    38-DEC-2000;
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                   01-DEC-2000
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human; autoimmune disease; Parkinson's disease; silicosis; gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia; immunosuppressive agent; adjuvant; enhance immune response; higher affinity antibody induction;
                                                                                                                                                                                                                                                                                     increased serum immunoglobulin concentration
ADB93844 standard; protein; 401 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0229344P.
2000US-0229345P.
2000US-0229509P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JAN-2001; 2001US-00764868
                                                                                             04-DEC-2003 (first entry)
                                                                                                                                          Human novel protein #78.
                                                                                                                                                                                                                                                                                                                                                                                       JS2002168711-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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05-SEP-2000;
08-SEP-2000;
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27-SEP-2000;
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2000US-0249299P

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The invention relates to an isolated polypeptide. The polypeptide is useful for diagnosing a pathological condition or a susceptibility to a pathological subject, by determining the presence or amount of expression of the polypeptide in a biological sample and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the condition based on the presence or amount of expression of the condition based on the presence or amount of expression of the condition based on the presence or amount of expression of the condition of a binding partner to the polypeptide is also useful for identifying a binding partner of effects an activity of the polypeptide. The polypeptide or the mucleic acid encoding the polypeptide is useful for preventing, treating, or ameliocating a medical condition, which involves administrating the polypeptide or the nucleic acid to a mammalian subject. The nucleic acid is useful for diagnosing a pathological condition or a susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or autoimmune disease, Parkinson's disease, alicosis, gastrointesting a utoimmune disease, atherosclerosis, haemophilia, thrombocytopenta. The polypeptide, the nucleic acid and the antibody are useful as immunosuppressive agents, the profession or a susceptibility antibody and incomment of the susceptibility and as agente to induce the profesor of a susceptibility or the pulpage of a susceptibility or the pulpage of a susc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence represents the amino acid sequence of a novel human protein. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format direct from USPTO at seqdata.uspto.gov/sequence.html?DocID=20020168711.
                                                                                                                                                                                                                                                                                                                                                                                New isolated polypeptide useful for diagnosing and treating immunosuppressive conditions such as autoimmune disease and Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; SEQ ID NO 701; 345pp; English.
                                                                                                                                                                                                                                     Barash SC;
08-DEC-2000, 2000US-0251856P.
08-DEC-2000, 2000US-0251868P.
08-DEC-2000, 2000US-0251869P.
                                                                                                                                                                                                                                  Rosen CA, Ruben SM,
                                                                                                               ROSEN C A.
RUBEN S M.
BARASH S C.
                                                                                                                                                                                                                                                                                            WPI; 2003-719985/68
                                                                                                                                                                                                                                                                                                                             N-PSDB; ADB93221.
                                                                                                               (ROSE/) F
(RUBE/) F
(BARA/) E
                                                                                                                                                                                                                                                                                                                                                                                                                                                disease.
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Sequence 401 AA;

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61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                87 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 146
                                                                                                                                                                                                                                121 NKADBEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                            9
                                                                                                                98
                                                                                                  27 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                            1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                      Gaps
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100.0%; Score 1105; DB 7; Length 401; 100.0%; Pred. No. 3.5e-108;
                                      0; Indels
                                                                                                                                                                                                                                                                                                            181 RMRASNELALAELEEEGKPEGPANSSKTCWC 212
                                      0; Mismatches
                                    Matches 212; Conservative
                  Local Similarity
Query Match
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AAB41604 standard; protein; 218 AA.

(first entry) 38-FEB-2001

Human ORFX ORF1368 polypeptide sequence SEQ ID NO:2736.

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;

Wulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;

Wulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;

W anticonvulsant; osteopathic; cagulant; vasotropic; antidiabetic;

W hypotensive; dermatological; immunosuppressive; antiinflammatory;

M antiviral; antibacterial; antifungal; antitheumatic; antiinflammatory;

antianaemic; gene therapy; cancer; proliferative disorder; hypertension;

M cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;

Cholesterol ester storage; systemic lupus erythematosus; infection;

Severe combined immunodeficiency; malaria; autoimmune disorder; asthma;

M allery; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;

M thrombosis; contraceptive.

Homo sapiens.

WO200058473-A2.

15-0CT-2000

31-MAR-2000; 2000WO-US008621.

02-APR-1999; 99US-0127636P. 05-APR-1999; 99US-0127728P. 30-MAR-2000; 2000US-00540763. 99US-0127607P, 11-MAR-1999;

(CURA-) CURAGEN CORP.

Leach M; Shimkets RA,

WPI; 2000-602362/57. N-PSDB; AAC75813. Novel nucleic acids and peptides derived from open reading frame X, disorders, useful for treating e.g. cancers, proliferative disorde neurodegenerative disorders and cardiovascular disease.

Claim 11; Page 1979-1980; 5507pp; English.

AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepacotropic; vulnerary; antiporiatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiporialit; indunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; indunotimulant; cardiant; intrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antirhenwalic; antiinflammatory; antibacterial; corp. or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative used to treat cancers, proliferative disorders, neurodegenerative disorders antibuts, hypertension, hypothyroidism, candiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive , AIDS, viral, bacterial or fungal infection, malaria, autoimmune

Sequence 218 AA;

Query Match

98.8%; Score 1092; DB 3; Length 218;

RMRASNELALAELEEEEGKPEGPANSSKTCWC 238

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a first to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal cubjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the
               ij
                                                                                              61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                  61 IMDTAGOERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                      174
                                                                                                                                                                                121 NKADEBOKROVGREOGOOKCPSLOLAKEYGMDFYETSACTNINIKESFTRLTELVLOAHR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                          9
                                                                    9
                                                          1 MAKQYDVLPRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKWKTIEVDGIKVRLQ
                                          1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                      121 NKADEEOKROVGREOGO-----OLAKEYGMDFYETSACTNINIKESFTRLTELVLOAHR
                 Gaps
                 9
               Indels
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                                                                                                                                                                                                                           KELEGLRMRASNELALAELEEEGKPEGPANSSKTCWC 218
 Pred. No. 3.4e-107;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                           ADES8127 standard; protein; 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page; 1017pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2002; 2002WO-US025765
  97.2%;
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                  Matches 212; Conservative
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       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus.
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Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis; liflammatory condition; sickle cell anaemia; hyperproliferative disorder; datorder; disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; isofaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AIDS; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymuclectide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNBFHSSHISTIGVDFKWKTIBVDGIKVRIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1077; DB 7;
Pred. No. 1.3e-105;
2; Mismatches 3;
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24-FEB-2000; 2000US-018454F.
02-MAR-2000; 2000US-0186350F.
16-MAR-2000; 2000US-0189874F.
17-MAR-2000; 2000US-0190076F.
18-APR-2000; 2000US-019123F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 212 AA;
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2000US-02262799
2000US-0226681P
2000US-0227182P
2000US-0229343P
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2000US-0229343P
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2000US-023943P
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2000US-0216880P.
2000US-0217487P.
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2000US-0220964P
2000US-0220964P
2000US-0224518P
2000US-022513P
2000US-0225214P
2000US-0225264P
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2000US-0241221P.
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21-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
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29-SEP-2000;
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29-SEP-2000;
20-SEP-2000;
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20-OCT-2000; 2000US-0241785P.
20-OCT-2000; 2000US-024180FP.
20-OCT-2000; 2000US-024180FP.
20-OCT-2000; 2000US-024180FP.
20-OCT-2000; 2000US-024180FP.
20-OCT-2000; 2000US-024182FP.
20-OCT-2000; 2000US-024647FP.
08-NOV-2000; 2000US-024647FP.
08-NOV-2000; 2000US-024647FP.
08-NOV-2000; 2000US-024647FP.
08-NOV-2000; 2000US-024652FP.
08-NOV-2000; 2000US-024920FP.
17-NOV-2000; 2000US-024921FP.
17-NOV-2000; 2000US-02511FP.
17-(HUMA-) HUMAN GENOME SCI INC 05-JAN-2001;

Ruben SM; Rosen CA, Barash SC, WPI; 2001-465460/50 N-PSDB; AAS27472. Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.

Claim 1; SEQ ID NO 1120; 880pp; English.

The invention relates to novel isolated polypeptides (I), and polymuclectides (II). (II) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune

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transplant rejections and graft versus host disease, infectious diseases transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and other blood-related disorders (sickle cell anaemia), myeloptoliferative disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. Gaucher's disease, Parkinson's disease), chromosomal abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (e.g. dafison's disease), reproductive system disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS), AAU17055-AAU17683 represent novel signal transduction pathway protein, amino acid
rheumatoid arthritis), inflammatory conditions, organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences of the invention
   X888888888888888888888
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61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                               84 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQXILIG 143
                                                                                 9
                                                                                                                     83
                                                                             1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                   24 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                           0; Gaps
75.3%; Score 832; DB 4; Length 188; 97.6%; Pred. No. 1.1e-79; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                            NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTR 164
     Query Match
Best Local Similarity 97.6
Matches 160; Conservative
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ADB94263 standard; protein; 188 AA 04-DEC-2003 (first entry) Human novel protein #497. ADB94263; ADB94263 XX AC ADB8 XXX DT 04-i DE WILL XXX XX HUMI XXW HIGH XXW HIGH XXX HOM XX RESULT 8

human; autoimmune disease; Parkinson's disease; silicosis; gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia; miumunosuppressive agent; adjuvant; enhance immune response; higher affinity antibody induction; increased serum immunoglobulin concentration.

Homo sapiens

US2002168711-A1

14-NOV-2002

17-JAN-2001; 2001US-00764868.

31-JAN-2000;

2000US-0180628P. 2000US-0214886P. 2000US-0216647P. 04-FEB-2000; 28-JUN-2000; 07-JUL-2000;

2000US-0216880P. 2000US-0217487P. 2000US-0217496P. 2000US-0218290P. 2000US-0220963P. 2000US-0220964P. 2000US-0224518P. 2000US-0224519P 14-AUG-2000; 14-AUG-2000;

14-AUG-2000; 2000US-0225757P.
14-AUG-2000; 2000US-0225757P.
13-AUG-2000; 2000US-0225758P.
22-AUG-2000; 2000US-022924P.
01-SEP-2000; 2000US-0229343P.
01-SEP-2000; 2000US-0229343P.
01-SEP-2000; 2000US-0229343P.
05-SEP-2000; 2000US-0229343P.
05-SEP-2000; 2000US-0229343P.
21-SEP-2000; 2000US-0229513P.
21-SEP-2000; 2000US-0239342P.
22-SEP-2000; 2000US-0239324P.
23-SEP-2000; 2000US-0236363P.
23-SEP-2000; 2000US-0236363P.
23-SEP-2000; 2000US-0236363P.
23-SEP-2000; 2000US-0236363P.
23-SEP-2000; 2000US-0236363P.
23-CCT-2000; 2000US-0236363P.
02-CCT-2000; 2000US-0237033P.
02-CCT-2000; 2000US-0237033P.
02-CCT-2000; 2000US-0237033P.
02-CCT-2000; 2000US-0237033P.
02-CCT-2000; 2000US-0237038P.
01-NOV-2000; 2000US-0244617P 2000US-0251869P 08-DEC-2000;

Rosen CA, Ruben SM, (ROSE/) ROSEN C A. (RUBE/) RUBEN S M. (BARA/) BARASH S C.

Barash SC

WPI; 2003-719985/68 N-PSDB; ADB93640 New isolated polypeptide useful for diagnosing and treating immunosuppressive conditions such as autoimmune disease and Parkinson's disease

Claim 11; SEQ ID NO 1120; 345pp; English

The invention relates to an isolated polypeptide. The polypeptide is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, by determining the presence or amount of expression of the polypeptide in a biological sample and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide is also useful for identifying a binding partner to the polypeptide; which involves contacting the polypeptide with a binding partner and determining whether the binding partner of the polypeptide. The polypeptide or the nucleic acid encoding the polypeptide is useful for preventing, treating, or ameliorating a medical condition, which involves administering the polypeptide is useful for preventing the polypeptide or the nucleic acid to a mammalian subject. The nucleic acid is useful for diagnosing a pathological condition or a susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition continue the presence or absence or the polypeptide are useful for treating

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disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide, the nucleic acid and the antibody are useful as immunosuppressive agents as adjuvants to enhance immune responses, and as agents to induce higher affinity antibodies and increase serum immunoglobulin concentrations. The protein. Note: The sequence data for this patent did not form part of printed specification but was obtained in electronic format direct from USPTO at seqdata.uspto.gov/sequence.thml?DocID=20020168711.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLiG176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
                                                                                                                                                                                                                                                                                                                                                                                 84 IMDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKMVSDVDEYAPEGVQXILIG 143
                                                                                                                                                                                                                                                                                                                                                              IMDTAGOERYQTITKQYYRRAQGIFLUYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                            MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHIGVDFKMKTIEVDGIKVRIQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                         1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                     0; Gaps
autoimmune disease, Parkinson's disease, silicosis, gastrointestinal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 38802; 21pp + Sequence Listing; English
                                                                                                                                                                                                              Score 832; DB 7; Length 188;
Pred. No. 1.1e-79;
0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 38802.
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97.6%;
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                Query Match 75.3
Best Local Similarity 97.6
Matches 160; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABL14773
                                                                                                                                                                                  Sequence 188 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pharmaceutical
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                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragmen derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent
                                                                                                                                                                           1 MAKKTYDLLFKLLLIGDSGVGKTCILFRFSDDAFTSTFISTIGIDFKIKTVELRGKKIKL
ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                          MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
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6
                                                                                            Length 204;
                                                                                                                           50; Indels
                                                                                               4
                                                                                            49.5%; Score 546.5; DB 4, 49.8%; Pred. No. 2.3e-49; iive 47; Mismatches 50
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                                                                                                                                                                                                                                                                                                                                                    180 LRMRASNELALAELEEEGKPEGPANSSKTC
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                           Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Woolf C, D'urso D,
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                                                                                             Query Match
Best Local Similarity
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                                                                Sequence 204 AA;
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that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating the injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed green that was obtained in electronic form directly from WIPO at
increases or decreases the expression of the polynucleotide sequence
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Sequence 207 AA;

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120
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                                                              1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                               61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG
                             0; Gaps
      49.3%; Score 545; DB 7; Length 207; 52.9%; Pred. No. 3.4e-49;
                            43; Indels
                             45; Mismatches
Query Match
Best Local Similarity 52.9%
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ABB11916 standard; peptide; 213 AA. 11-JAN-2002 (first entry) ABB11916; RESULT 11

Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; atharia; atharia; athariatory condition; proliferative retinopathy; atherosclerosis; coronary heart diseas; arterial isofaemis; bone disorder; osteoporosis; vascular growth disorder; is tissue respenzation; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antinifiammatory; antiasthmatic; antiarthritic; antiasteriosclerotic; ... Human rab8 homologue, SEQ ID NO:2286.

Homo sapiens

antifungal; vulnerary; antiulcer.

cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;

WO200157188-A2

09-AUG-2001.

05-FEB-2001; 2001WO-US003800.

03-FEB-2000; 2000US-00496914. 27-APR-2000; 2000US-00560875.

(HYSE-) HYSEQ INC

Tang YT, Liu C, Drmanac RT;

2001-457740/49.

Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis N-PSDB; ABA09160 and cancer

Claim 20; Page 276; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABB10981-ABB12330 represent nucleic acida encoding them. The equences ABA08225-ABA05374 represent nucleic acida encoding them. The chromation also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of detecting the nucleotides or the polypeptides in a sample, and methods of detecting the nucleotides or polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities and hence potential therapeutic applications. The polypeptides of the invention may have various activities; stem cell growth factor activity; have various activities; stem cell growth factor activity; immunodulatory activity; tissue growth activity; immunodulatory activity; tissue growth activity; immunodulatory activities; stem cell growth activity; immunodulatory activities; and activities, or may be now various activities; ancer cell proliferation or metastasis.

Cc dispetation activities; ancer cell proliferation or metastasis.

Cc chemotratic or chemokhrheit activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliocating medical conders, hasmatopoietic disorders (e.g., myabid or lymphoid cell promitions, e.g., by protein or gene therapy. Such conditions include cancers, hasmatopoietic disorders (e.g., myabid or lymphoid cell current is ischaemia, bone disorders (e.g., myabid or lymphoid cell cancers, hasmatopoietic disorders (e.g., myabid or lymphoid coll current is ischaemia, bone disorders (e.g., myabid or lymphoid coll cancers, hasmatopoietic disorders (e.g., myabid or lymphoid coll cancers, hasmatopoietic disorders (e.g., myabid or lymphoid coll cancers, hasmatopoietic sincerollers), and abnormal creativity er ethinopathy, atherosolerosis, concerns, hasmatopoietic disorders (e.g., myabid or lymphoid e.g., of burns, inclains and ulcers), while those with growth. For example, such polypeptides may be used

Sequence 213 AA;

ö 0; Gaps 49.3%; Score 545; DB 4; Length 213; 52.9%; Pred. No. 3.6e-49; ive 45; Mismatches 43; Indel8 Query Match Best Local Similarity 52.9%

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121 NKADEBOKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180

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further be used for gene therapy, chromosome mapping, in the identification of individuals and in forenaic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                  Sequence 221 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polymuciaculars, and incloudes and polymetrial and the use of ovarian antigen polymuciacotides and polymetrial and the use of orwarian antigens by treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorinea, infections (e.g., champida, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders (e.g., anaemia), cardiovascular disorders (e.g., anaemia), cardiovascular disorders cand urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may
                                                                                                                                                                                                                                                                                                                                                                                               ovarian cancer; breagt cancer; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst, dysmenorthosa; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forenisc analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological
      127 NKCDVNDKRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLARDIKAKMDKKLEGN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to to the sequences of the invention. The invention additionally relates to polynucleotides, antibodies against human ovarian antigen of ovarian antigens of ovarian antigens of ovarian antigens.
                                                                                                                                                                                                                                                                                                                                                                                  ovarian antigen; ovary; ovarian; breast; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                    Human ovarian antigen HCGMA67, SEQ ID NO:2465.
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                                                                                                                                                                                                    ABP41333 standard; protein; 221 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-2001; 2001WO-US018569
                                                  181 RMRASNE 187
                                                                                           187 SPQGSNQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birse CE, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-147878/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABQ54410.
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                                                                                                                                                                                                                                                                                           23-AUG-2002
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                                                                                                                                                                                                                                               ABP41333;
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                                                                                                                                       WDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGN 121
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                                                                                                                                                                                KADEEOKROVGREGGOOLAKEYGMDFYETSACTNLNIKESFTRLTELVLOAHRKELEGLR 181
                                                                                            75
                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                16 AKTYDYLFKLLLIGDSGVGKTCVLFRFSEDAFNSTFISTIGIDFKIRTIELDGKRIKLQI
                                                                2 AKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQI
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, pain, neuronal tissue, gene therapy,
spinal segmental nerve injury, chronic constriction injury, CCI,
spared nerve injury, SNI, Chung.
                                      ö
          Length 221;
                                    43; Indels
        48.9%; Score 540; DB 5; 52.7%; Pred. No. 1.3e-48; iive 45; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                          Human Protein P51153, SEQ ID NO 11024.
                                                                                                                                                                                                                                                                                                                                      ADE83429 standard; protein; 203 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-AUG-2001; 2001US-0312147P.
21-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-2002; 2002WO-US025765.
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
Query Match
Best Local Similarity 52.79
....hes 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Woolf C, D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-268312/26
                                                                                                                                                                                                                                        MRASNE 187
                                                                                                                                                                                                                                                                 196 POGSNQ 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAYER AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402003016475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENBANK; P51153
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caimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound or small molecule that regulates the extra polymucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the activity in an animal of one or more of the polypeptides given in the pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that animal seamental news in the preparing a medicament for treating a medicament for treating a medicament for treating a medicament for treating a medicament for preparing a medicament for treating a medicament for treating animal seamental seamental trainer of the polymucleotide or the compound that and a pharmaceutical promposition comprising a medicament for treating and animal seamental seamental for preparing a medicament for treating animal composition of the polymore.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKADEBOKROVGREGGOQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 47.6%; Pred. No. 8e-48;
Matches 100; Conservative 49; Mismatches 43; Indels 18; Gaps
or allelic variation of the nucleic acid sequence. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; pain; neuronal tiesue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RMRASNELALAELEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 GRRSGN-----GNKP--PSTDLKTC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Protein P51153, SEQ ID NO 3996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 203 AA;
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The invention discloses a composition comprising two or more isolated rat or human polynuclectides or a polynuclectide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynuclectide, a host cell comprising the vector is method for identifying a nuclectide sequence which is differentially regulated in an animal subjected to pain and a gent that increases or decreases the expression of the polynuclectide sequence that increases or decreases the expression of the polynuclectide sequence that is differentially expressed in neuronal tissue of a first animal composition and polynuclectide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for pain, a method for identifying a compound that regulates the expression of a polynuclectide sequence which is differentially expressed in an animal of one or more of the polypeptides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of polypeptides or their antibodies. The polynuclectide given in the specification, a method for identifying a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. spinal sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: the specification) but was obtained in electronic form directly from WIPO at seminors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NKADEBOKROVGREGGGOLAKEYGNDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAKQYDVI,FRLLLIGDSGVGKTCLLCRFTDNBFHSSHISTIGVDFKMKTIBVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 7; Length 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.1%; Score 532; DB 7; Length 203
47.6%; Pred. No. 8e-48;
ive 49; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RMRASNELALAELEEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 GRRSGN-----GNKP--PSTDLKTC 192
                                                                                                         Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB58196 standard; protein; 246 AA
                                                                                                           Befort K,
                                                                                                                                                                                                                                                                              Claim 1; Page; 1017pp; English
26-NOV-2001; 2001US-033347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 47.6%
Matches 100; Conservative
                                         (GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
                                                                                                           Woolf C, D'urso D,
                                                                                                                                                 WPI; 2003-268312/26.
GENBANK; P51153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 203 AA;
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(first entry)

14-MAR-2001

14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 14-AUG-2002; 2002WO-US025765

WO2003016475-A2 Ното варіепв

27-FEB-2003

Search completed: March 15, 2004, 11:14:51 Job time : 62 secs

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associated proteins represented in AABS8106 - AABS848. Lung cancer associated proteins and polynucleoride sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; cardioactive; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial cativity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences. The protein of lung cancer, chromosome captured in as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat diagnostic cardiovascular, renal, and proliferative disorders. The proteins may also cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18435 and peptide AABS849 are used in the course of the invention for the identification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 MAKAYDHLFKLLLIGDSGVGKTCLIRFAEDNFNNTYISTIGIDFKIRTVDIGGKKIKLQ 103
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                                                                                  cardioactive; immunomodulatory; muscular active; vulnerary; agatrointestinal; nephrotropic; antiinfective; synecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Indels 18; Gaps
                                                              cancer associated protein; neuroprotective; cytostatic;
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48.1%; Score 532; DB 3; Length 246;
Best Local Similarity 47.6%; Pred. No. 1.1e-47;
Matches 100; Conservative 49; Mismatches 43; Indels 1
                    Lung cancer associated polypeptide sequence SEQ ID 534.
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                                                                                                                                                                                                                                                                                                                         08-MAR-2000; 2000WO-US005918.
                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
(ROSE/) ROSEN C A.
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N-PSDB; AAF18072.
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March 15, 2004, 11:05:27; Search time 23 Seconds (without alignments) 475.857 Million cell updates/sec
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2: /cgn2 6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2 6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2 6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*
6: /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                          389414 segs, 51625971 residues
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                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length 1
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                        US-09-255-920A-14
US-09-075-454-3
US-09-075-454-3
US-08-9199-131-67
US-08-191-184-1
US-08-511-525-18
US-08-718-270A-52
US-08-718-270A-52
US-08-718-270A-52
US-08-76-551-6
US-09-255-920A-5
US-09-255-920A-5
US-08-718-270A-16
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,873
FILING DATE: Filed Herewith
CLASSIFICATION NATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0240 US
TELEPONMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08824873;
Sequence 4, Application US/08824873;
Patent No. S843717;
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl
TITLE OF INVENTION: NOVEL RAB PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
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TOPOLOGY: linear
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US-08-824-873-4
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STATE: C.
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-824-873-4
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63 DTAGOERYOTITKOYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNK 122
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                                                          61 IWDTAGQERFRTITTAYYRGAMGIMLVYDITNEKSFDNIRNWIRNIEEHASADVEKMILG 120
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                                     NKADEEOKROVGREOGOOLAKEYGMDFYETSACTNINIKESFTRLTELVLOAHRKELEGL
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                                                                                                                                                                                                                                                                                                      APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: Pincus, Matthew R.
APPLICANT: No. 58406831e, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action TITLE OF INVENTION: of P21 Ras
CORRESPONDENCE: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 205;
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MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,525
FILING DATE: 21-SEP-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.7%; Score 527.5; DB 2; 52.4%; Pred. No. 2.1e-50; iive 45; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 5370 Manhattan Circle, Suite 201 CITY: Boulder STRIE: Colorado COUNTRY: US
                                                                                                                                                                                                                               US-08-531-525-25

Sequence 25, Application US/08531525

Setent No. 5840683

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REPERENCE/DOCKET NUMBER: 37-
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 52...
Best Local 97; Conservative
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                                                                                                                                                         181 SPQGSNQ 187
                                                                                                                   181 RMRASNE 187
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                                                                                                                                                                                61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                      61 IWDIAGGERFRIITTAYYRGAMGIMLVYDIITNEKSFDNIRNWIRNIEEHASADVEKMILG 120
                                                                                                                                                           121 NKADEEQKROVGREGGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLOAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                             MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
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; Pred. No. 2.4e-52;
45; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/198,184
                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09198184
Patent No. 6010859
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl
TITLE OF INVENTION: NOVEL RAB PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0240 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/824,873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-02
TELECOMUNICATION INFORMATION:
TELEPHONE: 415.855-055
TELEPHONE: 415.855-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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Best Local Similarity 52.9%
Matches .99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                     181 RMRASNE 187
                                                                                                                                                                                                                                                                             181 SPOGSNQ 187
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CLONE: 234746
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61 INDIAGOERYQTITKOYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                       123 ADEEGKROVGREGGGQLAKEYGMDFYETSACTNLNIKESFTRLTELVLGAHRKELEGLRM 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKWKTIEVDGIKVRIQ
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                                                                                                                                                                                                                               Sequence 51, Application US/08531525
Patent No. 5840683
GENERAL INFORMATION:
APPLICANT: Hlavka, Joseph J.
APPLICANT: No. 58406831e, John F.
APPLICANT: No. 58406831e, John F.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action Manage OF Convention: Of P21 Ras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,525
FILING DATE: 21-SEP-1995
CLASSIFICATION: 50
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REFERENCE/DOCKET NUMBER: 37-94
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.9%; Score 518.5; DB 2;
55.0%; Pred. No. 2e-49;
tive 45; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Greenlee and Winner, P.C.
5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Canis familiaris US-08-531-525-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 94; Conserva
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                                                                                       183 RASNE 187
                                                                                                                              181 QGSNQ 185
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STATE: Colorade
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE
                                                                                                                                                                                                                    US-08-531-525-51
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  121 CDVNDKRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLARDIKAKMDKKLEGNSP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KTYDYLFKLLLIGDSGVGKTCVLFRFSEDAFNSTFISTIGIDFKIRTIELDGKRIKLQIW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIW 62
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                                                                                                                                                                                                                                                           APPLICANT: Hlavka, Joseph J.
APPLICANT: Hlavka, Matthew R.
APPLICANT: Pincus, Matthew R.
APPLICANT: No. 59104781e, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptidomimetics Inhibiting
TITLE OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,270A FILING DATE: 20-SEP-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 527.5; DB 2;
; Pred. No. 2.1e-50;
45; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Greenlee, Winner and Sullivan, P.C. STREET: 5370 Manhattan Circle, Sulte 201 CITY: Boulder STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION 514
PRIOR APPLICATION NUMBER: US 08/531,525
PRIOR DATE: 21-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,091
PRILNG DATE: 21-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                             Sequence 25, Application US/08718270A Patent No. 5910478 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REPERENCE/DOCKET NUMBER: 78-99
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 52.4%;
Matches 97; Conservative 45
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
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                                                                                       181 QGSNQ 185
                                              183 RASNE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM:
US-08-718-270A-25
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NAME/KEY: UNSURE
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ORGANISM: Mouse
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STREET: 5:
US-09-255-920A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKKTYDLLFKLLLIGDSGVGKTCYLFRFSDDAFNTFIS-IGIDFKKTYELQGKKKKLQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NKADEEOKROVGREOGOOLAKEYGMDFYETSACTNLNIKESFTRLTELVLO 171
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/718,270A

FILING DATE: 20-SEP-1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 08/531,525

FILING DATE: 21-SEP-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/531,525

FILING DATE: 21-SEP-1995

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                         Peptidomimetics Inhibiting
the Oncogenic Action of P21 Ras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 46.9%; Score 518.5; DB 2; Best Local Similarity 55.0%; Pred. No. 2e-49; Matches 94; Conservative 45; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                3: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle, Suite 201
                                                                                                                           APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: No. 59104781e, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptidomimetics
TITLE OF INVENTION: the Oncogenic A
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                             Sequence 51, Application US/08718270A Patent No. 5910478 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFRENCE/DOCKET NUMBER: 78-95
TELECOMMUNICATION INFORMATION:
TELEPAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                       STREET: 5370 Mar
CITY: Boulder
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                         80303
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-718-270A-51
                                             -08-718-270A-51
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RESULT

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60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQXILI 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONTION: (34)
CHER INFORMATION: The xaa at position 34 represents an unknown amino content information: acid.
US-09-255-920A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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APPLICANT: Pincus, Matthew R.
APPLICANT: No. 58406831e, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action TITLE OF INVENTION: OF P21 Ras
CORRESPONDENCE: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRL 165
                                                                                                 APPLICANT: LOTENS, James
APPLICANT: LOTENS, James
APPLICANT: Anderson, David
APPLICANT: Huang, Betty
APPLICANT: Huang, Betty
APPLICANT: Huang, Betty
APPLICANT: Shen, Mary
TITLE OF INVENTION: EXOL and EXO2, EXOCYTOTIC PROTEINS
FILE REFERENCE: A65905-1/DJB/RMS
CURRENT APPLICATION NUMBER: U5/09/255,920A
CURRENT APPLICATION NUMBER: 60/075,534
PRIOR APPLICATION NUMBER: 60/075,534
PRIOR PILING DATE: 1998-02-23
PRIOR FILING DATE: 1998-05-26
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 12
LENGTH: 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Indels
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COMPUTER: IBM PC compatible
OPERATS: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 46.7%; Score 515.5; DB 4; Best Local Similarity 56.0%; Pred. No. 4.4e-49; Matches 93; Conservative 41; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Greenlee and Winner, P.C.
5370 Manhattan Circle, Suite 201
Sequence 12, Application US/09255920A
Patent No. 6623980
GENERAL INFORMATION:
APPLICANT: FISHER, JOSEPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 35, Application US/08531525
Patent No. 5840683
GENERAL INFORMATION
APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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STATE: Colorade
COUNTRY: US
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62 DTAGQERFRITT-AYYRGAMGIMKV-DITNEKSFDNIKNWIRNIEBHASSDVERMILGNK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 DTAGQERYQTITIKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 ADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KTYDYLFKLLLIGDSGVGKTCLFFRFSEDAFNTTFISTIGIDFKIRTVELDGKKIKLQIW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 KQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 CDMNEKROVSKERGEKLAIDYGIKFLETSAKSSINVEEAFITLARDIMTKLNKKM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 46.4%; Pred. No. 9.8e-48;
Matches 96; Conservative 56; Mismatches 44; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: No. 58406831e, John P.
APPLICANT: No. 58406831e, John P.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action TITLE OF INVENTION: of P21 Ras
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 ---NENSLQEAVDKIKSPPKKPSQKKK 198
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                                                 FILING DATE: 21-SRP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,091
ATICHED DATE: 21-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-531-525-10
Sequence 10, Application US/08531525
Patent No. 5840683
GENERAL INFORMATION:
APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Mathew R.
APPLICANT: No. 58406831e, John F.
                                                                                                                                                                                  NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFRENCE/DOCKET NUMBER: 78-95
TELECOMMUNICATION INFORMATION:
TELEFROM (303) 499-8089
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Discopyge ommata US-08-718-270A-35
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MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
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STREET: 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 DTAGQERFRIIT-AYYRGAMGIMKV-DITNEKSFDNIKNMIRNIEEHASSDVERMILGNK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 CDMNEKRQVSKERGEKLAIDYGIKFLETSAKSSINVEEAFITLARDIMTKLNKKM---- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 ADEEOKROVGREOGOOLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KTYDYLFKLLLIGDSGVGKTCLLFRFSEDAFNTTFISTIGIDFKIRTVELDGKKIKLQIW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 KQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 45.6%; Score 503.5; DB 2; Length 207; Best Local Similarity 46.4%; Pred. No. 9.8e-48; Matches 96; Conservative 56; Mismatches 44; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: Pincus, Matthew R.
APPLICANT: No. 59104781e, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptidomimetics Inhibiting
TITLE OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---NENSLQEAVDKLKSPPKKPSQKKK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 RASNELALAE-LEEEGKPEGPANSSK 208
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,525
FILING DATE: 21-SEP-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTATION NUMBER: 33.878
REFERENCE/DOCKET NUMBER: 37-94
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SULT MALE.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,270A
FILING DATE: 20-SEP-1996
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 35, Application US/08718270A
Patent No. 5910478
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Discopyge ommata
US-08-531-525-35
                                                                                                                                                                                                                                                                                                                                                     LENGTH: 207 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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72 AGOER-RTITTAYYRGAMGILLVYDVTDESSFNNIRNWIRNIEQHASDNVNKILVGNKAD 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 -EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRMR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 YDYLIKLLIGDSGVGKSCLLLRFSDGSFTTSFITTIGIDFKIRTIELDGKRIKLQIMDT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: Pincus, Matthew R.
APPLICANT: Abajian, John F.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action TITLE OF INVENTION: of P21 Ras
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
BY 1015 DATE: US/08/531,525
PILING DATE: 21-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
.e-46;
54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 ASNELALAE-----LEEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 LSDTDSRAEPATIKISQTDQAAGAGQATQKSAC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
44.8%; Score 494.5;
Best Local Similarity 46.9%; Pred. No. 1e-4
Matches 100; Conservative 40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Greenlee and Winner, P.C.
5370 Manhattan Circle, Suite 201
PILING DAID:
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 60/004,091
FILING DATE: 21-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REPERENCE/DOCKET NUMBER: 78-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
TELEFRAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Arabidopsis thaliana
US-08-718-270A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34, Application US/08531525
Patent No. 5840683
                                                                                                                                                                                                                                                                                                            LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 -EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRMR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 YDYLIKLLIGDSGVGKSCLLLRFSDGSFTTSFITTIGIDFKIRTIELDGKRIKLQIMDT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              le-46;
nes 54; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

44.8%; Score 494.5; DB 2; Length 215;
Best Local Similarity 46.9%; Pred. No. 1e-46;
Matches 100; Conservative 40; Mismatches 54; Indels 19
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the Oncogenic Action of P21 Ras
52
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APPLICATION NUMBER: US/08/718,270A FILING DATE: 20-SEP-1996 CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/531,525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 ASNELALAE-----LEEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSDTDSRAEPATIKISQTDQAAGAGQATQKSAC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/08718270A
Patent No. 5910478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
PAPLICANT: No. 59104781e, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
                                                                 NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 37-9-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 anino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
            ATTORNEY/AGENT INFORMATION: NAME: Ferher Programmer NAME:
FILING DATE: 21-SEP-1995
                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boulder
STATE: Colorado
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
ORGANISM: Are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 80303
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DB 2;
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SOFWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,901
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
FILING DATE: FILED HEREWITH
FILING DATE: FILED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08916901
Patent No. 5892012
GENERAL INFORMATION:
APPLICANT: Hallman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Bal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                            REFERENCE/DOCKET NUMBER: 78-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
33,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Discopyge ommata
US-08-718-270A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                          194 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96; Conservative
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                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-916-901-3
                                                                                                                                                                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAXKTYDLLFKLLLIGDSGVGKTCVLFRFSDDAFNTTFISTIGIDFKIKTVELHGKKIKL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 GNK-DMEDKRVVLKSKGQ--IAEHAIRFFETSAKANINIEKAFLTLAEDILQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 GNKADEEOKROVGREGGOOLAKEYGMDFYETSACTNLNIKESFTRLTELVLO 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
44.2%; Score 488.5; DB 2; Length 194;
Best Local Similarity 55.8%; Pred. No. 4.1e-46;
Matches 96; Conservative 41; Mismatches 30; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34, Application US/08718270A

Patent No. 5910478

GENERAL INFORMATION:
APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: Abajian, Henry B.
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APPLICANT: Abajian, Henry B.
APPLICANT: Abajian, He
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle, Suite 201
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                  REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 37-94
REFERENCE/DOCKET NUMBER: 37-94
TELECOMMULCATION INFORMATION:
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/Me-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Discopyge ommata
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: siz
                                                                                                                                                                                                                                                                                                                                                                                                                linear
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STATE: Colorado
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: Die
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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61 QIWDTAGQERFHTIT-SYYRGAMGIMLVYDITNAKSFENISKWLRNIDEHANEDVERMLL 119
                                                                                                                                                                                                                                                   60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                               1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               120 GNK-DMEDKRVVLKSKGQ--IAEHAIRFPETSAKANINIEKAFLTLAEDILQ 168
                                                                                                                                                                                                                                                                                                                                                                           120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
Length 194;
                                                          41; Mismatches 30; Indels
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Ξ,
                                                                                                                                                                                                                                                                                                                                              61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                    121 NKADEEQKROVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                 1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                    5; Gaps
                                                                                                                                                              Length 201;
                                                                                                                                                        Query Match
43.3%; Score 478.5; DB 2; Length
Best Local Similarity 45.0%; Pred. No. 5.5e-45;
Matches 91; Conservative 42; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lal, Freeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCES: DOTTE: 1007te Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0367 US
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APPLICATION NUMBER: 08/916,901
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0367
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : :: | | | | 176 GAASGGERPNLKIDSTPVKPAG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 RMRASNELALAELEEEEGKPEG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09154602
Patent No. 6300472
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Carley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LIVRTUT04
; TYPE: amino acid
; STRANDEDRES: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBBARY: LIVRUT04
; CLONE: 2514506
US-08-916-901-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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121 NKSDLTTKKVVDNTTAKEFADSLGIPFLETSAKNATNVEQAF-----MIWAAEIKKRMGP 175
                                                                                                                                                                              61 IMDTAGOERYOTITKOYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                           1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
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                                       ; Score 478.5; DB 4.; Pred. No. 5.5e-45; 42; Mismatches 64.
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                                        43.3%;
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Best Local Similarity 45.03
Matches 91; Conservative
US-09-154-602-3
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1 MAKQYDVLFRLLLIGDSGVG.....LEBEBGKPBGPANSSKTCWC
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 2, Appli Sequence 701, App Sequence 5, Appli Sequence 4, Appli Sequence 4997, Ap Sequence 2465, Ap Sequence 534, App Sequence 1571, Ap Sequence 1571, Ap Sequence 8, Appli Sequence 600, Ap Sequence 600, Ap Sequence 600, Ap Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli
SUMMARIES	US-09-817-198A-2 US-09-817-198A-5 US-09-817-198A-5 US-09-817-198A-5 US-09-764-868-1120 US-10-369-493-4997 US-10-369-4465 US-09-925-300-1571 US-09-925-300-1571 US-09-925-300-1571 US-09-925-300-1571 US-10-128-714-3241 US-10-128-714-3241 US-10-128-714-3241 US-10-138-360-6 US-09-822-860-5
DB	
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Result No.	1 2 6 4 7 8 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

Sequence 766, App Sequence 193, Appli Sequence 193, Appli Sequence 6261, App Sequence 21876, App Sequence 21876, App Sequence 21876, App Sequence 150, App Sequence 150, App Sequence 150, App Sequence 150, App Sequence 150, App Sequence 150, App Sequence 15, Appli Sequence 15, Appli Sequence 13, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1106, App Sequence 1106, App Sequence 1106, App Sequence 1106, App Sequence 14, Appli Sequence 15, Appli Appli Appli Appli	Sequence 1, Appil Sequence 1738, Ap Sequence 67, Appl Sequence 67, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
        Sequence 2, Application US/09817198A

Patent No. US20020146758A1
GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
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Best Local Similarity 100.
Matches 212; Conservative
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ORGANISM: Human
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US-09-817-198A-2
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FEATURE:
MEMS/KEY: SITE
LOCAPION: (139)
OTHER INFORMATION: Kaa equals any of the naturally occurring L-amino acids
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                                                   121 NKADEBOKROVGREGGG-----QLAKEYGMDFYETSACTNINIKESFTRLTELVLQAHR 174
                                                                                                                                                                                                                                                                                                                                                                   FALCENT NO. USJUNGUL40/JOHAL
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REPERRICE: CLOOTIN8
CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT APPLICATION NUMBER: US/09/817,198A
SUFMER FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTERE OF OF Windows Version 4.0
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SOFTHARE: Patentin Ver. 2.0
SEQ ID NO 1120
LENGTH: 188
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT22
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
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                                                                                                                                                                                     181 KELEGLENKRASNELALAELEEEEGKPEGPANSSKTCWC 218
                                                                                                                                                      175 KELEGLEMRASNELALAELEEEEGKPEGPANSSKTCWC 212
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US-09-764-868-1120
i Sequence 1120, Application US/09764868
i Patent No. US20020168711A1
i GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09817198A
Patent No. US20020146758A1
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ORGANISM: Rattus norvegicus
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ORGANISM: Homo sapiens
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US-09-817-198A-4
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Sequence 5, Application US/09817198A

Patent No. US20020146758A1

GENURAL INFORMATION:

APPLICANT: YEJ Jane et al.

TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE

TITLE OF INVENTION: NUMBER: US/09/817,198A

CURRENT APPLICATION NUMBER: US/09/817,198A

CURRENT FILE OF ESEQ ID NOS: 33

SOFTWARE: FastSEQ for Windows Version 4.0

TYPE: PRT

TYPE: PRT
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                                                                                                                                    Sequence 701, Application US/09764868

Fatent No. US20020168711A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE ON INVENTION: NUMBER: US/09/764,868

CURRENT APPLICATION NUMBER: US/09/764,868

CURRENT APPLICATION DATE: 2001-01-7

Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 701

LENGTH: 401
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Pred. No. 5.2e-105;
0; Mismatches 0; Indels
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                       181 RMRASNELALAELEEEEGKPEGPANSSKTCWC 212
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Best Local Similarity 97.2%;
Matches 212; Conservative
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CORGANISM: Homo sapiens
US-09-764-868-701
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NAME/KEY: MISC_FEATURE
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ORGANISM: Homo sapiens
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US-09-925-302-534
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Sequence 4997, Application US/10369493

Sequence 4997, Application US/10369493

Sequence 4997, Application US/10369493

Sequence 4997, Application NS/10369493

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, 
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                       LOCATION: (164)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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                                        LOCATION: (151)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (188)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
75.3%; Score 832; DB 9; Length 188;
Best Local Similarity 97.6%; Pred. No. 3.9e-78;
Matches 160; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 NKADEEOKROVGREOGOOLAKEYGMDFYETSACTNLNIKESFTR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 NKADEEQXRQVGREQGQXLAXEYGMDFYETSACTNLNIKESFTR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-4997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 RMRASNELAL 190
                                                                                                                 NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-764-868-1120
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SEQ ID NO 3241
LENGTH: 206
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                                                                                                                                                                                                                                                                                                                         IMDTAGOERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                       1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
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                                                                                                                                                                                 18; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1571, Application US/09925300
; Sequence 1571, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
TILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR APPLICATION NUMBER: 601/24,270
; PRIOR PILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1899
; SEC ID NO 1571
                                                                                                                                         Length 246
                                                                                                                                       Query Match 48.1%; Score 532; DB 9; Length 24 Best Local Similarity 47.6%; Pred. No. 7.6e-47; Matches 100; Conservative 49; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 RMRASNELALAELEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 GRRSGN-----GNKP--PSTDLKTC 235
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 534
LENGTH: 246
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ORGANISM: Homo sapiens
US-09-925-300-1571
                                                                               ORGANISM: Homo sapiens
US-09-925-302-534
                                                              TYPE: PRT
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Sequence 8, Application US/09794257 Patent No. US20020009804A1 GENERAL INFORMATION:

US-09-794-257-8

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General information:

General information:

APPLICANT: Jiahkoff, Daniel

APPLICANT: Tishkoff, Daniel

APPLICANT: Zamudio, Carlos

APPLICANT: Zamudio, Carlos

APPLICANT: Zamudio, Carlos

APPLICANT: Lemieux, Sebastien M

TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and

TITLE OF INVENTION: Methods of Use

FILE REPERENCE: 10182-018-99

CURRENT PILING DATE: 2002-04-23

FRIOR APPLICATION NUMBER: US 60/285,697

FRIOR APPLICATION NUMBER: US 60/285,697

FRIOR APPLICATION NUMBER: US 60/285,890

FRIOR APPLICATION NUMBER: US 60/285,890

FRIOR APPLICATION NUMBER: US 60/303,899

FRIOR FILING DATE: 2001-06-05

FRIOR APPLICATION NUMBER: US 60/316,362

FRIOR APPLICATION NUMBER: US 60/316,362

FRIOR APPLICATION NUMBER: US 60/316,362

FRIOR FILING DATE: 2001-08-31

NUMBER OF SEQ ID NOS: 8603

SOFFWARE PALENT PALENT VALOR SEQ ID NOS: 8603

SOFFWARE PALENT PALENT VALOR SEQ ID NOS: 8603
TITLE OF INVENTION: 32705, 23224, 27423, 32700, 32712, No. US20020009804Alel TITLE OF INVENTION: Human G-Proteins FILE REFERENCE: 35800/209285 CURRENT APPLICATION NUMBER: US/09/794,257 PRIOR APPLICATION NUMBER: 60/185,606 PRIOR FILING DATE: 2000-02-27 PRIOR PILING DATE: 2000-02-29
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                                                                                                                                                                                                                                                                                                                                                                                                              207;
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58.7%; Pred. No. 5.1e-46;
tive 31; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                              DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                              47.8%; Score 528.5; DB 9 54.0%; Pred. No. 1.4e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47; Mismatches
                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 207
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3241, Application US/10128714 Publication No. US20030119013A1 GENERAL INFORMATION:
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; ORGANISM: Aspergillus fumigatus
US-10-128-714-3241
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Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 54.04
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: homo sapiens
US-09-794-257-8
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Galden, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APLICANT: APPLICANT: 2003-02-23
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: The Regents of the University of California TITLE OF INVENTION: Eukaryotic Genes Involved in Adult Lifespan Regulation TILE REFERENCE: 023070-11930US CURRENT APPLICATION NUMBER: US/01/19,766 CURRENT PILING DATE: 2002-06-24 PRIOR APPLICATION NUMBER: US 60/300,577 PRIOR APPLICATION NUMBER: US 60/300,577 PRIOR PILING DATE: 2001-06-22 PRIOR PILING DATE: 2001-06-25 PRIOR APPLICATION NUMBER: US 60/301,052 PRIOR FILING DATE: 2002-04-18 NUMBER OF SEQ ID NOS: 12 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.5%; Score 514; DB 14; Length 201;
46.9%; Pred. No. 4.2e-45;
ive 48; Mismatches 51; Indels 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: GTPase, gene T23H2.5
US-10-179-766-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5076, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
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Matches 100; Conservative
   APPLICANT: Murphy, Coleen
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ORGANISM: (
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Publication No. US20030119013A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Janay, Bo
APPLICANT: Tishhoff, Daniel
APPLICANT: Tishhoff, Daniel
APPLICANT: Eroshkin, Alexey M
APPLICANT: Eroshkin, Alexey M
APPLICANT: Eroshkin, Alexey M
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lamiel Daniel
APPLICANT: Lamidio Carlos
APPLICANT: Lamidio Carlos
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Low Number: US/10/128,714
CURRENT APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,890
PRIOR PLING DATE: 2001-04-27
PRIOR PLING DATE: 2001-04-27
PRIOR PLING DATE: 2001-04-27
PRIOR PLING DATE: 2001-06-31
PRIOR PLING DATE: 2001-06-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PRECENTIN VERSER: US 60/316,362
APPLOR PLING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
APPLICATION NUMBER: US 60/316,362
APPLICATION NUMBER: US 60/316,362
APPLICATION NUMBER: US 60/316,362
APPLICATION NUMBER: US 60/316,362
APPLICATION NUMBER: US 60/316,362
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5 RNYDFLIKLLLIGDSGVGKSCCLLRFSEDSFTPSFITTIGIDFKIRTIELDGKRVKLQIW 64
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58.7%; Pred. No. 5.1e-46;
tive 31; Mismatches 38;
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Hsu, Ao-Lin A.
Lehrer-Graiwer, Josh
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Best Local Similarity 58.7%
Matches 98; Conservative
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APPLICANT: Apfeld, Javier
APPLICANT: Dillin, Andrew
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ORGANISM: Aspergillus
US-10-128-714-8600
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GENERAL INFORMATION:
APPLICANT: ZHU, Shidoping et al.
TITLE OF INVENTION:
TITLE OF INVENTION: PROTEINS,
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/822,860
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 190
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
CURRENT BISCOPYGE OMMATA
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                                                                      61 QIWDTAGGERFHTITTSYYRGAMGIMLVYDITNAKSFDNIAKWLRNIDBHASEDVVKMIL 120
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Best Local Similarity 47.7%; Pred. No. 6.3e-45;
Matches 93; Conservative 52; Mismatches 42; Indels
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BC040679 Homo sapi
BC063736 Kanopus 1
BC013790 Mus muscu
BX640825 Homo sapi
BC033195 Danio rer
AB006189 Drosophil
AY060425 Drosophil
AY060425 Homo sapi
BT007184 Homo sapi
BT001185 Synthetic
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BC060015 Xenopus 1
AF48948 Homo sapi
M38390 Discopyge o
AF297660 Homo sapi
AF48945 Homo sapi
AF035646 Mus muscu
BC000896 Homo sapi
AF06691 Homo sapi
AF106691 Homo sapi
BC066374 Mus muscu
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BC052735 Mus muscu
BT001952 Arabidops
BT002186 Arabidops
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X56385 Canine rab8
BC002977 Homo sapi
AK025165 Homo sapi
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AF525280 Rattus no
BC020654 Homo sapi
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M83679 Sprague-Daw
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BC000799 Homo sapi
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AY042795 Arabidops
AY035132 Arabidops
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BD159881 Primer fo
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                                                                                                                                                                                                                             AX399903 Sequence
                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                             SUMMARIES
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BC027769
RATRABLSX
BC04679
BC063736
BC013790
HSM806937
BC053195
AX060425
AY606425
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BT008275
HSMRAB8
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BC000896
AF086917
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AF525280
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BC002977
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BC060015
AF498948
DYGORA1
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BC000799
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CFRAB10
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em_htg_inv:*
em_htg_other:*
em_htg_other:*
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em_htgo_hum:*
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                                              em_htg_pln: *
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Match Length DB
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2560
2210
1726
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2818
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888
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798
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-MODEL=frame+-pln.model -DEV=xlp
-MODEL=frame+-pln.model -DEV=xlp
-Gerz 1/USFTO spool p/US09817198/runat 15032004_101746_20542/app_query.fasta_1.391
-B=GenEmbl -QFWT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UOTALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OTTEMT=pto -NORM=ext -HEAPSIZE=560 -MINLEN=0-MAXLEN=200000000
-USER=US09817198_@CGN 1 1_5265_@runat 15032004_101746_20542 -NCPU=6 -ICPU=3
-NO_MMAP -LARREQUERY -NGG SCORES=0 -WAATT -BSPBAELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDEXT=7
                                                               March 21, 2004, 11:03:18; Search time 2744 Seconds (without alignments) 3348.660 Million cell updates/sec
                                                                                                                           ......LEEEEGKPEGPANSSKTCWC
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                               OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                         3470272 seqs, 21671516995 residues
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1 MAKQYDVLPRLLLIGDSGVG.
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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gb_htg: *
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Contact: nisc mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Grannite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                       BCO27769
Mus musculus RAB15, member RAS oncogene family, mRNA (cDNA clone MGC:38375 IMAGE:5345297), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                  501 AAGGAGTATGGCATGGACTTCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAG
                                                                      SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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                                                                                                                                                                                                                                                            GluGlyProAlaAsnSerSerLysThrCysTrpCys 212
                                                                                                                                                                                                                                                                                          681 GAGGGCCCAGCGAACTCTTCGAAAACCTGCTGGTGC 716
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Mus musculus
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Strausberg, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            500
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                                   PAT 06-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 ATGGCGAAGCAGTACGATGTGCTGTTCCGGCTGCTGCTGTTCGGGGACTCCGGGGTGGGC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang, Y.T., Asundi, V., Zhou, P., Xue, A.J., Ren, F., Zhang, J., Wang, J.R., Zhao, Q.A., Wang, D., Liu, C., Drmanac, R.T. and Wehrman, T. Nucleic acids and polypeptides
Patent: WO 0218424-A 74 07-MAR-2002;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Matches:
Conservative:
Mismatches:
Indels:
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Sequence 74 from Patent WO0218424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                              ROD 27-APR-1993
                                                                                                                                                                                                                                181 ArgMetArgAlaSerAenGluLeuAlaLeuAlaGluLeuGluGluGluGluGluGlyLysPro 200
  121 AsniysalaaspGluGluGlniysargGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
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                                                                                                                628 AAGGAGTACGGCATGGACTTCTACGAACAAGTGCCTGCACCAACCTTAATAATAAAGAG 687
                                                                                                                                                      SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu 180
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                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Original source text: Rattus norvegicus (strain Sprague-Dawley) (library: LAMBDA ZAPII) adult brain cDNA to mRNA.
Location/Qualifiers
1. 945
                        Elferink, L.A., Anzai, K. and Scheller, R.H.
rabls, a novel low molecular weight GTP-binding protein
specifically expressed in rat brain
J. Biol. Chem. 267 (9), 5768-5775 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                          RATRAB15X 945 bp mRNA linear RC
Sprague-Dawley (clone LRB9) RAB15 mRNA, complete cds.
M83679
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LMW GTP-binding protein.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 55 Row: d Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19527265. Location/Qualifiers
                                                                                                                                                                                                                                                ATTTGGGACACAGCAGGCAGGAGGACTACCAGACTATCACAAAGCAGTACTATCGGCGA 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGTGGGTCAGTGACGTGGATGAGTACGCTCCAGAAGGAGTCCAGAAGAACTCCTAATTGGG
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MetAlaLysGlnTyrAspValLeuPheArgLeuLeuLleGlyAspSerGlyValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCCAGGGAATATTTTTAGTCTACGACATTAGCAGTGAGCGCTCCTATCAGCATATCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229. .720
/note="RAB; Region: Rab subfamily of small GTPases"
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                              CGAP_Mam6"
                                                                                                                                                                                                                                                                                                                                                                      'note="Vector: pCMV-SPORT6
                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="LocusID:104886"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-817-198C-2 (1-212) x BC027769 (1-3139)
                                                                                                                                                                                                                                                                                                                                                lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                          gene="Rab15"
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99.53%
98.11%
98.64%
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                                                                                                                                                                                                                                                                                                                                                                                            gene
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UNIH-MGC Project URL: http://mgc.nci.nih.gov
On Sep 16, 2003 this sequence version replaced gi:26251822.
Ontact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
TobnA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
TOSHiyuki and Piero Carninci (RIKEN)
TOSHiyuki and Piero Carninci (RIKEN)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
Info@bcgsc.Dc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readdman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lilsa Prabhu, Parvaneh Saedein, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorre, Miranda Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon start=1
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/db_xref="C1:26787"

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Location/Qualifiers
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                 Submitted (29-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26. .343
hotte="RAB; Region: Rab subfamily of small GTPases"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3326
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/lab_host="DH10B"
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="RAB15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .3326
/organism="Homo sapiens"
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82.42%
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94.89%
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Strausberg, R.
Direct Submission
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                              PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
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COMMENT
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                                                                                                                                                                                                              JOURNAL
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Homo sapiens RAB15, member RAS onocogene family, mRNA (cDNA clone
MGC:42319 IMAGE:4817835), complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 ArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluCluGluGluGluGluGlyLysPro 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly 120
                                                                                                       280 AAGACCTGCCTGCTATGCCGCTTCACCGACAACGAGTTCCACTCCTCGCATATCTCCACC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 artregeacacaecaecaecaecaecaecraccaecrarcacaaaacaeracracceecea 459
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                             41 IleGlyValaspPheLysMetLysThrIleGluValaspGlyIleLysValargIleGln 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MetalaLysGlnTyrAspValLeuPheArgLeuLeuLeulleGlyAspSerGlyValGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 GluGlyProAlaAsnSerSerLysThrCysTrpCys 212
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VERSION
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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Wax, S.I., Wang, J., Haieh, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, W.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Boask, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Qunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergen, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y.
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schen, S.J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Ligor. Eachhologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-DEC-2003) National Institutes of Health, Xenopus (Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4801, Rockville, MD 20892-7510, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'clone="MGC:68722 IMAGE:4057038"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Xenopus laevis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project
Contact: XGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
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Klein, S. and Strausberg, R.
     (bases 1 to 2348)
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  REFERENCE
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnileLysGluSerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGlu 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuGluGlyLeuArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGlu 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 AAGACCTGCTGCTGTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACC 124
                                                                                                                                                                                                                                                                                                                                             ATCGGTGTTGACTTTAAGATGAAGACCATAGAGGTAGACGCCATCAAAGTGCGGATACAG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 GGGTGCCTCACCGGGGAAGGCAAGGCGAGGGCCAGATGGGAAGGCAAATGCTTCCAGGAA 423
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae; Xenopus.
1 (bases 1 to 2348)
Klein,S.L., Strausberg,R.L., Wagner,L., Pontius,J., Clifton,S.W. and Richardson,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete cds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
                                                                                                                                                                                                                                                                                                                                                                                                      61 IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424 GCTTTGCCTTCCACAGCCCTGGATGAAGACCTCTGGTACGCACCAGAAGGCGTCCAGAAG
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                                                                                                                    5 ATGGCGAAGCAGTACGATGTGCTGTTCCGGCTGCTGCTGATCGGGGACTCCGGGGTGGGC
                                                                                                                                                                            LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 AAGTGGGTCAGTGACGTGGATGA-GGTAGGAGATGCCACCTCACTGCCGGGGTGTGGAGA
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Xenopus laevis cDNA clone MGC:68722 IMAGE:4057038,
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US-09-817-198C-2 (1-212) x BC040679 (1-3326)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musnaria; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musnaria; Lubaesa 1 to 2560)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausberg, R.L., Zeaberg, B., Buter, C.M., Schuler, G.D., Altschul, S.F., Zaeberg, B., Buterow, K.H., Schaefer, C.F., Batt, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haich, F., Diatchenko, L., Maruslana, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonddo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., McKernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Mulak, J.A., Gunzarne, P.H., Richards, S., Sanchez, A., Whiting, M., Sodergren, E.J., Lu, X., Gibbs, R.A., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodrigues, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Sonnerch, A., Schein, J.E., Sonnerch, M., Schein, J.E., Sonnerch, M., Schein, J.E., Sonnerch, M., Schein, J. S., and Marra, M. J., Wang, D. M., Mannerch, M., Schein, J. S., and Marra, M. J., Mannerch, A., Whiting, M., Green, E.D., Lu, M., Mannerch, M., Schein, J.E., Sonnerch, M., Schein, J. S., A., Mannerch, M., Schein, J. S., A., Mannerch, M., Schein, J. S., Sonnerch, M., Schein, J. S., Sonnerch, M., Schein, J. Sonnerch, M., Schein, J. Sonnerch, M., Schein, J. Sonnerch, M., Schein, J. Sonnerch, M., Schein, J. Sonnerch, M., Schein, J. Sonnerch, M., Schein, J. Sonnerch, M., Schein, J. Sonnerch, M., Schein, J. Sonnerch, M., Schein, J. S., Sonnerch, M., Schein, J. Sonnerch, M., Schein, J. Sonnerch, M., Schein, J. Sonnerch, M., Schein, J. Sonnerch, M., Schein, J. Suadias, S. Sonnerch, M., Schein, J. Sonnerch, M., Schein, J. Son
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 5 Row: i Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19527265.
Location/Qualifiers
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Direct Submission
Submitted (04-SEP-2001) National Institutes of Health, Mammalian Submitted (04-SEP-2001) Cancer Gene Collection (MGC), Cancer Gene Collection (MGC), Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Email: cgapbs-r@mail.nih.gov
Itsue Procurement: Gilbert Smith, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCN-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Mus musculus RAB15, member RAS oncogene family, mRNA (cDNA clone
MGC:6897 IMAGE:2655151), complete cds.
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558 TTCAAACATTGAACATTGATTGGACCATGAACTAAAGGAGGAAAT-CTCGCAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
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/note="RAB; Region: Rab subfamily of small GTPases"
/db_xref="CDD:cd00154"
  ASDVDEYAPDGVQKILIGNKADEEQKRQVGKNQGLKAMFKH"
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Bequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone DKFZp686J06205) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="human fetal brain" /clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host DH10B; sites SfiIA + SfiIB" /dev stage="fetal" 1. .210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="CPRPOGGRNCOPLRLEAVAPEACVRDKSRGVDFKMKTIEVDGIK
VRIQIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEVGDATS
LPGCGEGASPGKARRGPDGKANASRKLCLPQPWMKTSG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similarity to GTP-binding protein rab15 (Rattus norvegicus)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlnGly11ePheLeuValTyrAsp11eSerSerGluArgSerTyrGlnHis11eMetLys
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Matches:
Conservative:
Mismatches:
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/protein_id="CAE45901.1"
/db_xref="GI:34365091"
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                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="14q23.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="DKFZp686J06205"
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VSDVDEYAPGGVQKILIGNKADEEQKRQVGREQGQQLAKEYGMDFYETSACFFSFFS
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1 (bases 1 to 2210)
Bloecker, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wilemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 ATCGGTGTTGACTTTAAGATGAAGACTATCGATGTAGACGCCATCAAAGTGAGAATACAG 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
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107		clone distribution: MGC clone distribution information can be found through the 1.M.A.GE. Consortium/Link at: http://image.llnl.gov Series: IRAK Plate: 117 Row: g Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF Location/Qualifiers analysis, Similarity but not identity to protein. Location/Qualifiers 1. 1726 / organism="Danio rerio" //mol_type="minna" paraon:7955" / clone="MGC:64010 IMAGE:6792909" / clone="MGC:64010 IMAGE:6792909" / clone="MGC:64010 IMAGE:6792909" / clone="WgC:64010 IMAGE:6792909" / clone="WgC:64010 IMAGE:6792909" / clone="WgC:64010 IMAGE:6792909" / clone="WgC:64010 IMAGE:6792909" / clone="Wcctor: pCMV-SPORT6.1" / lab_host="MI10E" / lab_host="MI10E" / lab_host="MI10E" / product="Unknown (protein for MGC:64010)" / product="Unknown (protein for MGC:64010)" / protein id="AAH33195.1" / db_xref="GI:31419201" / kranslation="MAKKYDPFEKILLIGDSGVGKTCLIRFAEDNFNSTYISTIGID / kranslation="MAKKYDPFEKILLIGDSGVGKTCLIRFAEDNFNSTYISTIGID / kranslation="MAKKYDPFEKILLIGDSGVGKTCLIRFAEDNFNSTYISTIGID / kranslation="MAKKYDPFEKILLIGDSGVGKTCLIRFAEDNFNSTYISTIGID / kranslation="MAKKYDPFEKILLIGDSGVGKTCLIRFAEDNFNSTYISTIGID / kranslation="MAKKYDPFEKILLIGDSGVGKTCLIRFAEDNFNSTYISTIGID / kranslation="MAKKYDPFEKILLIGDSGVGKTCLIRFAEDNFNSTYISTIGID / kranslation="MAKKYDPFEKILLIGDSGVGKTCLIRFAEDNFNSTYISTIGID / kranslation="MAKKYDPFEKILLIGDSGVGKTCLIRFAEDNFNSTYISTIGID / kranslation="MAKKYDPFEKILLIGDSGVGKTCLIRFAEDNFNSTYISTIGID / kranslation="MAKKYDPFEKILLIGDSGNGKTCLIRFAEDNFNSTYISTIGID / k	Alignment Scores: Score: Score: Score: Score: Score: Score: Score: Score: 563.50 Matches: 107 Score: 107 Score:
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	ATGAATTAGTTCCAAGTCTTCCCTGTGAGCAGCTTCTTTCCTGAAATCTTGGGACCAGGT GGAGTTGCAAGATTGGGATCTAGTCCTGTGAGATTGTTGGTGTGTGGACCAGGT CCATTTGAATCCTTGGGTCCCCAGTTCCTGTAGAATGAGGTTGGACTTAGAAG TCTTCTACCCTAAGCTCTCCCGTGATACCCAAGGAAGAGCGACCAGAGG I	137 GlnGlnLeualalysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeu	

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AY060425
AY060425.1 GI:16648397
FLI_CDNA.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster (fruit fly)
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera, Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophila.
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                                                                                                                                                                                                                  161 SerPheThrArgLeuThr---GluLeuValLeuGlnAlaHisArgLys------Glu 176
                                                                          AlaGlnGly1lePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
                                                                                                        694
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                                                                                                                                                                                                                                                           LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
                                                                                                                                                                                                                                                                                                                                                                                                                  993
                                             634
                                                                                                                                                                                                                                                                                                                                                                                  177 LeuGluGlyLeuArgMetArgAlaSerAsnGlyLeuAlaLeuAlaGluLeuGluGluGlu 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-AUG-1997) Koichi Ozaki, Osaka University, Graduate School of Science, Department of Biology; 1-1 Machikaneyama, Toyonaka, Osaka 560, Japan (E-mail:ozaki@bio.sci.osaka-u.ac.jp, Tel:+81-6-880-5439, Rax:+81-6-850-5439)
               GTCTGGGACACAGGACAGGAGGGTTTAAGACCATCACCACTGCATACTACAGAGGG
                                                                                                                                      LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly
                                                                                                                                                                                                  AsniysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endoptertygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster mRNA for Rab10, complete cds.
AB006189
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Rab proteins of Drosophila melanogaster: novel
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/organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="Oregon R"
/db_xref="taxon:7227"
/tissue_type="head"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rab-protein family FEBS Lett. 404 (1), 65-69 (1997)
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AB006189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF498943 624 bp mRNA linear PRI 01-MAY-2002
Homo sapiens small GTP binding protein RAB8 (RAB8) mRNA, complete
100 MetLysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIle 119
                                                                                                                                                                                                                                                                        120 GlyasniyaalaaspGluGluGlniysargGlnValGlyargGluGlnGlyGlnGlnLeu 139
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Catarrhini, Hominidae; Homo.
                                                                                                                                                                               2 (bases 1 to 624)
Publ,H.L. III, Ikeda,S.R. and Aronstam,R.S.
Direct Submission
Submitted (05-APR-2002) CDNA Resource Center, Guthrie Research Institute, One Guthrie Square, Sayre, PA 18840, USA
Location/Qualifiers
                                                                 60 GlnIleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hc
1 (bases 1 to 624)
Publ, H.L. III, Ikeda, S.R. and Aronstam, R.S.
Homo sapiens RAB family small GTP binding protein RAB8
Unpublished
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/note="RAB family member"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tisgue_type="brain"
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AF498943.1 GI:20379061
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This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcription of unspliced precursor RNAs, and reverse transcription about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trānslation="MAKKTYDLLFKLLLIGDSGVGKTCILFRFSDDAFTSTFISTIGI
DKKKTVELEGKKKIKLOIMDTAGQBRFHTITTSYRGAMGINLYDITNBKSFENIYK
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RAFCELABAILDKTSGRESARNQERVIIDRRNQEKAPGYSKCCA"
                     Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J., Chawe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C. J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Li, C., Lewis, S. E., Rubin, G.M. and Celniker, S.
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                                                                                                                                                   Submitted (19-00T-2001) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA Sequence submitted by:

Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
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Matches:
Conservative:
Mismatches:
Indels:
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/db_xref="GI:16648398"
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
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Location/Qualifiers
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gene="Rab10"
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Xalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinga, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.

Direct Submission

Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA collection of human full length This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) clonins system between the Sall and HindlII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindlII site to maintain reading frame.

Clone distribution: http://bioinfo.clontech.com/orfclones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="mel transforming oncogene (derived from cell line NKI4) - RAB8 homolog" /protein id="AAP35848.1" /b. xref="GI:3058320" /t.ranslation="MAKTYDYLFKLLIGDSGVGKTCVLFRFSEDAFNSTFISTIGID fr.ranslation="MAKTYDYLFKLLIGDSGVGKTCVLFRFSEDAFNSTFISTIGID KRYRTIELOKRIKLQIMPAGQERFRITTATYRGAMGIMLYVDITNEKSFDNIRNW IRNIERHSAADVERGHIGHKCDVMDKRQVSKERGEKLALDYGIKFMETSAKANINVEN AFFTLARDIKAKMDKKLEGNSPQGSNQGVKITPDQQKRSSFFRCVLL"
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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1 (bases 1 to 624)
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Parmer,A.
Cloning of human full-length CDSs in BD Creator(TM) System Donor
IRNIEEHASADVEKMILGNKCDVNDKRQVSKERGEKLALDYGIKFMETSAKANINVEN
AFFTLARDIKAKMDKKLEGNSPQGSNQGVKITPDQQKRSSFPRCVLL"
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Homo sapiens mel transforming oncogene
NK14)- RABB homolog mRNA, complete cds.
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Matches:
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Editaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Butaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 660)
Zahraoui,A., Joberty,G., Arpin,M., Fontaine,J.J., Hellio,R., Tavitian,A. and Louvard,D.
A small rab GrPess is distributed in cytoplasmic vesicles in non polarized cells but colocalizes with the tight junction marker ZO-1 in polarized epithelial cells
J. Cell Biol. 124 (1-2), 101-115 (1994)
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rab-related GTP-binding protein.
Homo sapiens (human)
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Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.

Direct Submission

Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full length cypression clones generated by BD Biosciences Clontech and the Harvard Institute of Froteomics. Bach CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been the Sall and HindlII sites of the pDNR-DUAL vector. Additional sequences in the clone: "ACC' after Sall site and before Ang' to provide Kozak consensus sequence; 'GG' after last codon and before HindlII site to maintain reading frame.

Clone distribution: http://bloinfo.clontech.com/orfclones.
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/transl_table=11
/transl_table=11
/transl_table=11
/product="Homo sapiens mel transforming oncogene (derived from cell line NK14)- RAB8 homolog"
/protein id="AAP36967.1"
/db xxef="G1:3058589"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthetic construct synthetic construct synthetic construct artificial sequences.

artificial sequences.

1 (bases 1 to 624)

Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y., Chening of human full-length CDSs in BD Creator(TM) System Donor
                                                                                                                                                                                                                                                                                                                                               SYN 13-MAY-2003
oncogene (derived
                                                                         141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
                                                                                                                 480
                                                                                                                                                     161 SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu 180
                                                                                                                                                                                           540
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                                                                                                 BT008275 624 bp mRNA linear S' Synthetic construct Homo sapiens mel transforming once from cell line NK14) - RAB8 homolog mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH5alpha T1 resistant"
/note="Vector: pDNR-Dual"
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note="Mutations: 623:Stop->Leu"
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                                                                                                                                                                                                                                   181 ArgMetArgAlaSerAsnGlu 187
                                                                                                                                                                                                                                                                                                                                                                                                                           BT008275.1 GI:30585388
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AFFILARDIKAKMDKKLEGNSPQGSNQGVKITPDQQKRSSFFRCVLL"
                                                                                                                                                              gene family
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg 80
                                                                                                                                                                                                                                                                        Chavrier, P., Vingron, M., Sander, C., Simons, K. and Zerial, M. Molecular cloning of YPT1/SEC4-related cDNAs from an epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
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                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (17-AUG-1990) Zerial M., EMBL, Meyerhofstrasse 1,
                                                                                                                                                               protein transport; ras gene; ras
                                                                                         760 bp mRNA linear M
rab8 mRNA for ras-related GTP-binding protein.
                                                                                     linear
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                   571
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::: ||||||:::
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Canis familiaris
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GCATTTTTCACTCTCGCCAGAGATATCAAAGCAAAAATGGACAAAAATTGGAAGGCAAC 550
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               Direct Submission
Submitted (26-NOV-1990) A. Zahraoui, INSERM-U 248, 10 AVENUE
VERDUN, 750-10 PARIS, FRANCE
Location/Qualifiers
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Matches:
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81 AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
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                                                                                                                                                                141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnlleLysGlu 160
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Add17370 |
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Add17377
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Wehrman T;
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Wang D, Liu C, Drmanac RT,
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                          Human cDNA SEQ ID NO
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WO200218424-A2.
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Zhao QA,
ABQ9336:
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Command line parameters:

-MODEL=frame+ p21.mcdel -DEV=xlp
-MODEL=frame+ p21.mcdel -DEV=xlp
-Q=/CQ=1/USPTO spool p/US09817198/runat_15032004_101745_20514/app_query.fasta_1.391
-Q=/CQ=1/USPTO spool p/US09817198/runat_15032004_101745_20514/app_query.fasta_1.391
-DEN Geneseq 29Jan04 -QFWR=fastap -SUPFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LIST=6 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=65 -DOCALIGN=200 -THR RAX=100 -THR MIN=0 -ALIGN=15
-MODEL-CCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09817198 @CGN 1 1 708 @runat_15032004_101745_20514 -NCFU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NGG_SCORES=0 -MALT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XCAPOP=10 -XCAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Human CDN
Human Ras
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CDNA enco
Human CDN
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                                                                             (without alignments)
2544.119 Million cell updates/sec
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                                                                                                                           1 MAKQYDVLFRLLLIGDSGVG......LEBEEGKPEGPANSSKTCWC
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                                                                  March 21, 2004, 11:01:53 ; Search time 354 Seconds
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          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                         2124099041 residues
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Maximum Match 100%
Listing first 45 summaries
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AAD47168
AAC75813
AAS27472
ADB93650
ABL27707
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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genesegn2004s:*
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AAS27053 standard; cDNA; 2021
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19-MAY-2000; 2
07-JUN-2000; 2
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24-FEB-2000;
02-MAR-2000;
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14-AUG-2000;
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17-MAR-2000;
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                                                                                                                                                                                                                AAS27053
                                                                                                                                                                                      RESULT
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                                                                                                                                                                                                                            The invention relates to an isolated polynucleotide (I) comprising one of administering to a mammalian subject a condition comprising administering to a mammalian subject a composition comprising manipulatering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).

(I) a useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                               New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetAlaLysGlnTyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 AAGACCTGCTGCTGTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1054 BP; 240 A; 314 C; 304 G; 195 T; 0 U; 1 Other;
                                                                                                                                                                                      Claim 22; SEQ ID NO 74; 284pp + Sequence Listing; English
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Matches:
Conservative:
Mismatches:
Indels:
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antilifiammatory; anti-HIV, antibacterial; antilifiammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlbS; ss; acquired immune deficiency syndrome.
181 ArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLysPro 200
                                                                                           Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding novel signal transduction pathway protein, Seq ID 88
                                                                                                                                                                                                                                                                        681 GAGGCCCAGCGAACTCTTCGAAAACCTGCTGGTGC 716
                                                                                                                                                                                                             201 GluGlyProAlaAsnSerSerLysThrCys 212
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08-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
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14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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08-NOV-2000;
08-NOV-2000;
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14-SEP-2000;
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14-SEP-2000;
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21-SEP-2000;
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Rosen CA, Barash SC, Ruben SM; 17-NOV-2000; 2000US-0249212P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249215P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249269P.
17-NOV-2000; 2000US-0249269P.
17-NOV-2000; 2000US-024930P.
17-NOV-2000; 2000US-024930P.
17-NOV-2000; 2000US-024930P.
17-NOV-2000; 2000US-025103P.
05-DEC-2000; 2000US-025103P.
06-DEC-2000; 2000US-025104P.
06-DEC-2000; 2000US-025104P.
06-DEC-2000; 2000US-025106P.
05-JAN-2001; 2001US-0259678P (HUMA-) HUMAN GENOME SCI INC WPI; 2001-465460/50. P-PSDB; AAU17136.

Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.

Claim 1; SEQ ID NO 88; 880pp; English.

The invention relates to novel isolated polypeptides (1), and

C polymucleotides (II). (I), (II) and the antibody to (I) are useful for

diagnosing, preventing and treating diseases including immune system

disorders (e.g. congenital and acquired immunodeficiencies, autoimmune

Cd disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ

C transplant rejections and graft versus host disease, infectious diseases

C transplant rejections and graft versus host disease, infectious diseases

CC transplant rejections and graft versus host disease, infectious diseases

CC gaucher: a disease, parkinson's disease), myeloproliferative disorders

CC disorders, primary haematopoietic disorders, hyperproliferative disorders

CC disorders, primary haematopoietic disorders, incromosomal abnormalities

CC Altheimer's disease, Parkinson's disease), chromosomal abnormalities

CC Altheimer's disease, parkinson's disease), chromosomal abnormalities

CC Altheimer's disorders, dermatological disorders (e.g. Arthythmial),

C respiratory disorders, dermatological disorders (e.g. Addison's

CC disease), reproductive system disorders, gastrointeetinal disorders

CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of

CC (inflammatory disorders) pathogens, activators of T-cells, to induce

CC higher affinity antibodies, and as a means to induce tumour proliferation

CC higher affinity antibodies, and as a means to induce tumour proliferation

CC higher affinity antibodies, and as a means to induce tumour pathologies

CC AASZ7850 represent novel signal transduction pathway protein coding

CC sequences and PCR primers of the invention

2021 212 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 8.95e-118 1105.00 100.00\$ 100.00\$ Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB: Pred. No.: Score:

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Rosen CA,
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(BARA/) 1
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                                                                141 AAGACCTGCCTGTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCCACC
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                                                   LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
                  MetalaLysGlnTyrAspValLeuPheArgLeuLeuLleGlyAspSerGlyValGly
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                                                                                                                                                                                                                                                                                                                                                                                 GluGlyProAlaAsnSerSerLysThrCysTrpCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                increased serum immunoglobulin concentration
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 US-09-817-198C-2 (1-212) x AAS27053 (1-2021)
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2000US-0180628P.
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04-FEB-2000; 2
28-JUN-2000; 2
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## 11.702.2000 | 200008-0217456P.
## 11.702.2000 | 200008-0217456P.
## 11.702.2000 | 200008-0217456P.
## 14.702.2000 | 200008-0212559P.
## 14.702.2000 | 200008-021259P.
## 14.702.2000 | 200008-021259P.
## 16.702.2000 | 20008-021259P.
## 16.702.2000 | 2
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acid encoding the polypeptide is useful for preventing, treating, or ameliorating a medical condition, which involves administering the polypeptide or the nucleic acid to a mammalian subject. The nucleic acid is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, which involves determining the presence or absence of amutation in The nucleic acid, and diagnosing a pathological condition or susceptibility to a pathological condition based on the presence or absence of the mutation. The polypeptide, the nucleic acid and an antibody to the polypeptide are useful for treating autoimmune disease, Parkinson's disease, allicosis, gastrointestinal disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide, the nucleic acid and the antibody are useful as immunosuppressive agents, as adjuvants to enhance immune responses, and as agents to induce higher affinity antibodies and increase serum immunoglobulin concentrations. The present sequence represents cDNA encoding a novel human protein. Note: the sequence date for this patent did not form part of the printed specification but was obtained in electronic format direct from USPTO at segdata.uspto.gov/sequence.html?DocID=20020168711.

Sequence 2021 BP; 464 A; 564 C; 553 G; 440 T; 0 U; 0 Other;

81 AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100 101 LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly 120 41 IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln 60 ATCGGTGTTGACTTTAAGATGAAGACCATAGAGGTAGAGGGGATCAAAGTGCGGATACAG 261 ATCTGGGACACTGCAGGGCAGGAGATACCAGACCATCACAAAGCAGTACTATCGGCGG GCCCAGGGGATATTTTGGTCTATGACATTAGCAGCGGAGCGCTCTTACCAGCACATCATG 21 LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr 61 IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg 381 AAGTGGGTCAGTGACGTGGATGAGTACGCACCAGAAGCCGTCCAGAAGATCCTTATTGGG Length: Matches: Conservative: Mismatches: Indels: Gaps: US-09-817-198C-2 (1-212) x ADB93231 (1-2021) 8.95e-118 1105.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Alignment Scores: 321 Query Match: DB: 셤 8 g 8 g ò 셤 ò 셤 ઠે d 8

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immunodeficiency; recorded and alzheimer's disease; cirrhosis; Parkinson's disease; wasting disease; cachexia; myocardial infarction; Parkinson's disease; wasting disease; cachexia; myocardial infarction; osteoporosis; atherosolesons; glomerulonephritis; Crohn's disease; irritable bowel syndrome; multiple solerosis; osteoarthritis; allergy; pancreatitis; autoimmune thyroiditis; rheumatoid arthritis; osteopathic; Sjogren's syndrome; infection; transgenic; gene therapy; nootropic; gout; neuroprotective; vasotropic; cytostatic; dermatological; nephrotropic; ophthalmological; tranquilliser; cancer; stroke; Grave's disease; AIDS; asthma; anaemia; drug screening; gene; ss.
                                                                                                                                Human; Ras-like protein; inflammation; cell proliferation; apoptosis;
                                                                                                                                                                                                                                                                                                                                 "Human Ras-like protein"
681 GAGGCCCAGCGAACTCTTCGAAAACCTGCTGGTGC 716
                                                                                                          Human Ras-like protein encoding cDNA.
                                                                                                                                                                                                                                                                            Location/Qualifiers
                                          AAD47168 standard; cDNA; 3257 BP
                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-2002; 2002WO-US009328.
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                                AAD47168
                     RESULT
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New isolated human Ras-like protein polypeptide, useful for diagnosing, treating or preventing inflammation and disorders associated with cell proliferation and apoptosis, e.g. AIDS, cancer, allergies, anemia, asthma Ye J, Di Francesco V, Beasley EM; WPI; 2003-018913/01 P-PSDB; AAE29096. or stroke. Gan W,

(PEKE) PE CORP

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AsniysAlaAspGluGluGluGlniysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 441 AATAAGGCTGATGAGGAGCAGAAACGCCAGGTGGGAAGAGAGCAAGGGCAGCAGCTGGCG LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnlleLysGlu

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Claim 4; Page 73-74; 82pp; English.

The invention relates to human Ras-like protein and its corresponding nucleic acid. The Ras-like protein and DNA is useful in the development of human therapeutics and diagnostic compositions. They are useful in the diagnosis, prevention and treatment of inflammation and disorders associated with cell proliferation and apoptosis, e.g. AIDS and other infectious or genetic immunodeficiencies, neurodegenerative disease e.g. Alzheinmer's disease, Parkinson's disease, wasting disease e.g. cachaxia, ischaemic injury, toxin-induced diseases such as alcohol-induced liver damage or injury, toxin-induced diseases such as alcohol-induced liver damage or cirrhosis, osteoporosis or ancer. They are also used to treat disorders associated with inflammation including allergies, atopic dermatitis, atherosclerosis, asthma, anaemia, Crohn's disease, diabetes mellitus, Grave's disease, glomerulonephritis, gout, irritable bowel syndrome, untoindumune thyroiditis, rheumatoid arthritis, sjogren's syndrome, autoimmune thyroiditis, rheumatoid arthritis, sjogren's syndrome, uveitis, trauma, or viral, bacterial, fungal, parasitic, protozoal or belminthic infections. The antibodies of the invention are useful in

620

SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu 180

501 AAGGAGTATGGCATGGACTTCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAG 560

CGGATGCGTGCCAGCAATGAGTTGGCACTGGCAGAGCTGGAGGAGGAGGAGGAGGAGAAACCC 680

621 201

GluGlyProAlaAsnSerSerLysThrCysTrpCys 212

181 ArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGluGlyLysPro 200

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pharmacogenomic analysis or for tissue typing. The transgenic animals are useful for studying the function of a Ras-like protein, and identifying and evaluating modulators of its activity. Ras-like protein is used in drug screening assays and its DNA is used in gene therapy. The present sequence is human Ras-like protein encoding cDNA
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Other; Sequence 3257 BP; 793 A; 892 C; 870 G; 702 T; 0 U; 0

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Length:
Matches:
Conservative:
Mismatches:
Indels:
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         1.71e-117
1105.00
100.00%
100.00%
                                          Best Local Similarity:
                                Percent Similarity:
Alignment Scores:
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US-09-817-198C-2 (1-212) x AAD47168 (1-3257)

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ArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLysPro 200
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GAGGGCCCAGCGAACTCTTCGAAAACCTGCTGGTGC 680 AAC75813 standard; cDNA; 1666 (first entry) 08-FEB-2001 645 AAC75813; g

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; Human ORFX ORF1368 polynucleotide sequence SEQ ID NO:2735.

antiviral; antibacterial; antifungal; anti vulnerary; antipsoriatic; antiparkinsonian; nootropic, neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; thrombosis; contraceptive; ss

Homo sapiens,

WO200058473-A2.

05-OCT-2000

31-MAR-2000; 2000WO-US008621

31-MAR-1999; 99US-0127607B. 02-APR-1999; 99US-0127636B. 05-APR-1999; 99US-0127728P. 30-MAR-2000; 2000US-00540763.

CURA-) CURAGEN CORP.

Leach M; Shimkets RA,

WPI; 2000-602362/57. P-PSDB; AAB41604

× Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.

5; Page 1978-1979; 5507pp; English.

AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX compared to a sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthriti; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; cardiant; antifungal; antiheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORRX-associated disorder. The mucleic acids can be used to express ORRX proteins in gene therapy vectors. The proteins and nucleic acids may be cased to treat cancers, proliferative disorders, neurodegenerative disorders, proliferative disorders, neurodegenerative closeders cardiovascular disease, cdiabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune cartialed changes, aplastic anaemia, burns, wounds, bone and cartialed canders, aplastic anaemia, burns, wounds, bone and cartialed canders. enhance coagulation; to inhibit thrombosis; and as a contraceptive

461 G; 341 T; 0 U; 2 Other; Sequence 1666 BP; 333 A; 529 C;

1666 212 0 0 6 Matches: Conservative: Mismatches: Indels: Length: 2.21e-116 1092.00 97.25% 97.25% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: Score:

US-09-817-198C-2 (1-212) x AAC75813 (1-1666)

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2000US-0232398P
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31-JAN-2000; 2
04-FBB-2000; 2
02-MAR-2000; 2
16-MAR-2000; 2
117-MAR-2000; 2
119-MAR-2000; 2
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14-SEP-2000;
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25-SEP-2000;
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  antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlbS; ss; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                             391 AAGTGGGTCAGTGACGTGGATGAGTACGCACCAGAAGGCGTCCAGAAGATCCTTATTGGG 450
                                                                      210
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                                                                                                                                                                                                                                                                                                                                                                                                           AACCTCAACATTAAAGAGTCATTCACGCGTCTGACAGAGCTGGTGCTGCAGGCCCATAGG 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  690
                                                                                                                                                                                                                      331 GCCCAGGGGATATTTTTGGTCTATGACATTAGCAGCGCGCTCTTACCAGCACATCATG 390
                                                                                                                                                                                                                                                                                                                                                                                                                                            LysGluLeuGluGlyLeuArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGlu 194
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                                                                                                                         ATCGGTGTTGACTTTAAGATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAG
                                                                                                                                                                       Arcricegacacrecagededededagaraccacaccarcacaaaccacrararcegeee
                                                                                                                                                                                              AlaGlnGly1lePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHislleWet
                                                                                                                                                                                                                                              LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly
                                                                                                                                                                                                                                                                                                                                             ------GlnLeuAlaLysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThr
                                                                                                                                                                                                                                                                                                                                                           631 AAGGAGCTGGAAGGCCTCCGGATGCGTGCCAGCAATGAGTTGGCACTGGCACTGGCAGAG
   Met AlaLysGlnTyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyValGly
                         91 Aregegaageagraceargrecrerrecegerecrecrearcegeaacrecegeregee
                                                 LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
                                                                         AAGACCTGCCTGCTGTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACC
                                                                                               IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArg1leGln
                                                                                                                                            lleTtpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrIysGlnTyrTyrArgArg
                                                                                                                                                                                                                                                                                              AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGln-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding novel signal transduction pathway protein, Seq ID 507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluGluGluGlyfysProGluGlyProAlaAsnSerEserLysThrCysTrpCys 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGAGGAGGCCAAACCCGAGGGCCCAGCGAAACCTTCGAAAACCTGCTGGTGC 744
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Rosen CA, Barash SC, Ruben SM; (HUMA-) HUMAN GENOME SCI INC. WPI; 2001-465460/50. P-PSDB; AAU17555.

Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune

The invention relates to novel isolated polypeptides (I), and definition relates to novel isolated polypeptides (I), are useful for polynucleotides (II). (II) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. chewatoid arthritis), inflammatory conditions, organ transplant rejections and graft versus host disease, infectious diseases (e.g. transplant rejections and graft versus host disease, infectious diseases (e.g. bepatitis C), bleeding disorders, haemoglobin abnormalities and other blood-related disorders (sickle cell anaemia), myeloproliferative disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (e.g. Addison's epithelial cell proliferation, endocrine disorders (e.g. Addison's chisease), reproductive system disorders (cirrhosis), as stimulators of thigher affinity antibodies, and as a means to induce tumour proliferation (in pathologies e.g. acquired immune deficiency syndrome (AIDS). AASZ6976-AASZ7850 represent novel signal transduction pathway protein coding sequences and PCR primers of the invention Claim 1; SEQ ID NO 507; 880pp; English. disorders and neuronal disorders.

lignment Scores:				
red. No.:	6.91e-87	Length:	266	
core:	832.00	Matches:	160	
ercent Similarity:	97.56%	Conservative:	0	
est Local Similarity:	97.56%	Mismatches:	4	
uery Match:	75.29%	Indels:	0	
B: 5	4	Gaps:	0	

US-09-817-198C-2 (1-212) x AAS27472 (1-566)

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186T-/T8-60	U9-8I/-I98C-Z (I-ZIZ) X AASZ/4/Z (I-S06)	
	MetAlaLysGlnTyrAspValLeuPheArgLeuLeuLeuLleGlyAspSerGlyValGly 20	0
7.1	ATGGCGAAGCAGTACGATGTGCTGTTCCGGCTGCTGCTGATCGGGGACTCCGGGGTGGGC 13	130
21	LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerFisIleSerThr 40	0
131	ABGACCTGCCTGCTGTGTGTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACC 19	190
41	IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln 60	0
191	ATCGGTGTTGACTTTAAGATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAG 25	250
61	IleTrpAspThrAlaGlyGluGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg 80	0
251	ATCTGGGACACTGCCAGGGCAGGGAGATACCAGACCATCACAAAGCAGTACTATCGGCGG 31	310
81	AlaGlnGly1lePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 10	100
311	GCCCAGGGGATATTTTGGTCTATGACATTAGCAGCGAGCG	370
101	LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly 12	120
371	AAGTGGGTCAGTGACGTGGATGAGTACGCACCAGAAGGCGTCCAGAASATCCTTATTGGG 43	430
121	AsnLysalaAspGluGluGluGlnLysArgGlnValGlyArgGluGlnGlnGlnGlnLeuAla 14	140
431	AATAAGGCTGATGAGGAGCAGAWACGGCAGGTGGGGAAGAGAGAAGAGGCAAGCGCANCTGGCG 49	490
141	LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 16	160
491	AANGAGTATGGCATGGACTTCTATGAAACAAGTGCCTGCACCAACCTNAACATTAAAGAG SS	550
161	SerPheThrArg 164	
551	TCATTCACGCGT 562	

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The invention relates to an isolated polypeptide. The polypeptide is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, by determining the presence or amount of expression of the polypeptide in a biological ample and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide is also useful for identifying a binding patrner to the polypeptide is also useful for identifying a binding patrner and determining whether the binding patrner effects an activity of the polypeptide. The polypeptide or the nucleic acid encoding the polypeptide is useful for preventing the polypeptide or the nucleic acid encoding the polypeptide. The polypeptide or the nucleic acid condition, which involves administering the polypeptide or the nucleic acid to a mammalian subject. The nucleic acid is useful for diagnosing a pathological condition or a susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or ausceptibility to a pathological condition or aucceptibility to the polypeptide are useful for treating auccimument disease, Parkinson's disease, silicosis, gastrointestinal concentrations, the nucleic acid and the antibody are useful as immunosuppressive agents, as adjuvants to enhance immune responses, and as agents to induce affinity antibodies and increase serum immunosuppressive agents or affinity antibodies and increase serum immunosupore afficient on a succeptibility antibodies and increase serum immunosupore processive agents or affinity antibod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 ATGGCGAAGCAGTACGATGTGCTGTTCCGGCTGCTGCTGATCGGGGACTCCGGGGTGGGC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 AAGACCTGCCTGCTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 ATCGGTGTTGACTTTAAGATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAG 250
                                                                                                                                                                                                              New isolated polypeptide useful for diagnosing and treating immunosuppressive conditions such as autoimmune disease and Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetalaLysGlnTyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 LysThrCysLeuCysArgPheThrAspAsnGluPheHisSerKeisIleSerThr
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Matches:
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08-DEC-2000; 2000US-0251868P.
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                                                                                                                                                            WPI; 2003-719985/68
                                                  (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C
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                                                                                                                                                                                           ss; gene; human; autoimmune disease; Parkinson's disease; silicosis; gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia; immunosuppressive agent; adjuvant; enhance immune response; higher affinity antibody induction; increased serum immunoglobulin concentration.
                                                                                                                                                             Human cDNA encoding a novel protein #497.
                                                  ADB93650 standard; cDNA; 566 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US - 0224519P

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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; ofmentexis; chemokinesis; thrombolysis; orrogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; atherosclerosis; coronary heart disease; arterial ischaemia, bone disorder; osteoporosis; vascular growth disorder; ischaemia, tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antianiamatory; antiathmatic; antiarthritic; haemostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 LeuArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLys 199
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                                                                                                                                                                                                                                     257 Ardecaaadaaaaccraccarrrecrerrraaacrerrecrearcegrearreagaere 316
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               Conservative:
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546.50
72.04%
49.76%
49.46%
               Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                        141 LysGluTyrGlyMetAspPheTyrGluThrSerAlacysThrAsnLeuAsnIleLysGlu
                                                                                                                                                                                                                                                                            ATCTGGGACACTGCAGGGCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGG
                                                                                                                                                                                 121 AsniysAlaAspGluGluGluGlnIysArgGluValGlyArgGluGlnGlyGlnLeuAla
                                                                                                                                                                                                                     AATAAGGCTGATGAGGAGCAGAWACGGCAGGTGGGAAGAGAGCAAGGGCAGCANCTGGCG
                                                            LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly
                                     AlaGlnGly1lePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster genomic polynucleotide SEQ ID NO 34594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1540 BP; 437 A; 353 C; 420 G; 330 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 34594; 21pp + Sequence Listing; English.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                         TCATTCACGCGT
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ABL2770

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179

784

865

New

1540

Length:

Alignment Scores: Pred. No.:

736

919

919 139

496

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79

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39

Gaps:

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Sequences ABB10981-ABB12310 represent 1350 novel human polypeptides, and cequences ABB10981-ABB12310 represent nucleic caids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the linvention, methods of geneting the nucleotides of antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of detecting the nucleotides or polypeptides in a sample, and methods of dentifying compounds which proplypeptides of the invention have homology to known proteins, thereby giving an linsight into their probable biological activities, and hence collypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, days various activities, stem cell growth factor activity, have various activities, stem cell growth factor activities, memunomodulatory activities; stem cell growth factor activities, memunomodulatory activities, the memostatic or the invention are useful for preventing, treating or ameliorating medical convocances, cortemorates, cortemora
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 805; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                  Liu C, Drmanac RT;
                                                                                                                                                                                                                                      03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
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                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
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                                                                                                       40200157188-A2
                                                                 Homo sapiens
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cc may also be used in the diagnosis of the above conditions, and in drug cc screening techniques. The present sequence represents a cDNA encoding a XX cover luman polypeptide of the invention cover lu

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199 ATATGGGACACAGGGGGTCAGGAACGGTTTCGGACGATCACAACGGCCTACTACAGGGGT 258
                                                                                                                                                                                                                                                            AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
                                                                                                                                                                                                                                                                           121 AsniysAlaAspGluGluGluIysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 SerPheThrArgieuThrGluLeuValLeuGlnAlaHisArgiysGluLeuGluGlyLeu 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoes; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; genstrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytosteatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
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                                                                                    LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr 40
                                                                                                                                             IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
                                                                                                                                                                                                     61 ileTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
                            Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ovarian antigen HCGMA67 cDNA, SEQ ID NO:290.
US-09-817-198C-2 (1-212) x ABA09160 (1-1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 ArgMetArgAlaSerAsnGlu 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             559 AGCCCCCAGGGGAGCAACCAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABQ54410 standard; cDNA; 2411 BP.
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polybrucleorides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens, and the use of polymucleorides, antibodies against human ovarian antigens, and the use of ovarian antigens, and the use of conditions include ovarian cancer and breast cancer, and disorders. Such conditions include ovarian cancer and breast cancer, and catestatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, and sorders (e.g., infertility, disorders of pregnancy, anovulation, calsorders, infertions (e.g., chlamydia, HIV, toxoplasmosis, and toxic disorders, infertions (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome, ovarian cysts, and dysmenorrhoea), endocrine ciscoportics, auctimenume cophoritis, systemic lupus erythematosus, closucers (e.g., anaemia), cardiovascular disorders (e.g., anaemia), cardiovascular disorders (c.g., anaemia) and the collection of individuals and in forensic analysis
                                                                                                                                                                                                                                                                                     useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                                                                                                                             Isolated nucleic acid molecules encoding novel ovarian polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2411 BP; 600 A; 671 C; 583 G; 547 T; 0 U; 10 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 290; 2922pp; English.
07-JUN-2000; 2000US-0209467P
                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                   Rosen CA;
                                                                                                                                                                        WPI; 2002-147878/19.
P-PSDB; ABP41333.
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GGAATTGACTTTAAAATTAGGACCATAGAGCTCGATGGCAAGAGAATTAAACTGCAGATA 226
                                                                                                                                                                     ACCTGTGTCCTGTTCCGCTTCTCCGAGGACGCCTTCAACTCCACTTTTATCTCCACCATA 166
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                                                                                                                                                                                                              ThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThrIle 41
                                                                                                                                                                                                                                                                                                                                    TrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArgAla
                                                                                                                                                     2 AlalysGlnTyrAspValleuPheArgLeuLeuLeuIleGlyAspSerGlyValGlyLys
                                                                                                                                                                                                                                                                         GlyValAspPhelysMetLysThrileGluValAspGlyIleLysValArgIleGlnIle
                            98
4 4 5
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              Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                       US-09-817-198C-2 (1-212) x ABQ54410 (1-2411)
              3.44e-52
540.00
76.88%
52.69%
48.87%
                                            Percent Similarity:
Best Local Similarity:
Alignment Scores:
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Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; and immunomodulatory; muscular active general; vulnerary; gastrointestinal activity in ephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardioactive; immunomodulatory; muscular active; vulnerary; asstrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural antibacterial; diagnosis; neural proliferative disorder; wound halling; infectious disease; ds.
                      287 ATGGGCATCATGCTGGTCTACGACATCACCAACGAGAAGTCCTTCGACAACATCCGGAAC 346
                                                                                                      406
                                                                                                                                                                                                                   161
                                                                                                                                                                                                                                                                                                            82 GlnGlyllePhereuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMetLys 101
                                                                                                                                                                              407 AAGTGTGATGTGAATGACAAGAGACAAGTTTCCAAGGAACGGGGAGAAAAGCTGGCCCTC 466
                                                                                                                                               122 LysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLys 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders
                                                                                          467 GACTATGGAATCAAGTTCATGGAGACCAGCGGAAGGCCAACAACGTGAGAAAATGGA
                                                                                                                                                                                                                                                                                         162 PheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArg
                                                                                                                                                                                                                     142 GluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSer
                                                                      102 TrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGlyAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer associated protein; neuroprotective; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                   182 MetArgAlaSerAsnGlu 187
                                                                                                                                                                                                                                                                                                                                                                                                   587 CCCCAGGGAGCAACCAG 604
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              identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat disorders such neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and peptide AABS8549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein sequences
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  sequences may be used for detection of lung cancer,
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AAA40104 standard; cDNA; 716 BP

AAA40104 ID AAA

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This invention describes a novel human Rablo cDNA sequence. The protein coded by said sequence belongs to Yap/Rab family and is the homolog of mouse Rablo. The present invention also relates to the polypeptide coded by said nucleotide sequence and the application and preparing process of said polynucleotide and said polypeptide. This sequence encodes the human Rablo protein described in the method of the invention
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                                                                                Human; Rablo; Yap/Rab family; ss
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215 ACCATAGGAATAGACTTCAAGATCAAAACAGTTGAATTACAAGGAAAGAAGATCAAGCTA 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel human Rablo cDNA sequence. The protein coded by said sequence belongs to Yap/Rab family and is the homolog of mouse Rablo. The present invention also relates to the polypeptide coded by said nucleotide sequence and the application and preparing process of said polynucleotide and said polypeptide. This sequence encodes the human Rablo protein described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGCGAAGAAGAAGACGTACGACCTTGTTTTCAAGCTGCTCCTGATCGGGGATTCCGGAGTG 154
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 GlyAsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeu 139
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                                                             ThrileGlyValAspPheLysMetLysThrileGluValAspGlyIleLysValArgile
                     Preparation of human gene coding sequence, its encoded polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 861 BP; 258 A; 189 C; 200 G; 214 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                              Human; Rab10; Yap/Rab family;
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                                                                                                                                                         313 CAGATATGGGATACAGCAGGCCAGGAGCGATTTCACACCACCATCACTACTACTACAGA
                                                                                                                                                                                                                                                                    MetAlaLysGln---TyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyVal
                                             GlyLysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSer
                                                                                        193 GGGAAGACCTGCGTCCTTTTTCGTTTTTCGGATGATGCCTTCAATACCACCTTTATTTCC
                                                                                                          ThrileGlyValAspPheLysMetLysThrileGluValAspGlyIleLysValArgile
                                                                                                                                               GlnIleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; GTPase; GTP binding; gene therapy; cancer;
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127. .729
                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of human RAB10.
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/product= "RAB10"
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P-PSDB; AAB19165.
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                                                                                                                                                              The present sequence encodes a mammalian RAB protein. RAB proteins constitute the largest family of small GrPases, with over 40 identified isoforms. RAB proteins contain four highly conserved peptide sequences involved in GTP binding and hydrolysis. Compositions comprising RAB nucleic acid are useful for identifying homologous or related genes, in producing compositions that modulate the expression or function of RAB, for gene therapy, mapping functional regions of the protein and in studying associated physiological pathways. In addition, modulation of the gene activity in vivo is used for prophylactic and therapeutic purposes, such as treatment of cancer, and identification of cell type based on expression. The DNA may also be used to identify expression of the gene in a biological specimen
Novel isolated nucleic acid encoding a mammalian RAB protein useful for identifying homologous or related genes, in producing composition that modulates expression or function of RAB for cancer therapy.
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Job time : 362 secs
                                                                                                                 Claim 4; Page 38-39; 58pp; English.
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66, Appl 28, Appl 49, Appl 1096, Ap 4, Appli 1060, Ap 387, Appli 4, Appli

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US-09-399-913-66
US-08-888-077A-28
US-09-976-594-1096
US-09-976-594-1096
US-09-016-434-1060
US-09-016-434-1159
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US-09-016-434-1124
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US-09-3120-587-138
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ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Disketter
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,901
FILING APPLICATION DATA:
APPLICATION NUMBER:
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NAME: Billings, Lucy J.
RGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-916-901-4

Sequence 4, Application US/08916901

Patent No. 5892012

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti

APPLICANT: Carley, Nell C.

APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: RAB PROTEINS NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharma
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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Command line parameters:
-MODEL=frame+ p3n.model -DEV=xlp
-MODEL=frame+ p3n.model -DEV=xlp
-MODEL=frame+ p3n.model -DEV=xlp
-Cgnz 1/USFTO spool p/US09817198/runat 15032004 101743 20457/app_query.fasta_1.391
-DB=Issued_PatenTe_B NA -QFMT=fastap -SUPFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=51ts -START=1 -END=-1 -MATRIX=blosmac2 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE-pct -THR MAR_100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=pcc -NORM=ext -HEAPSIZE=500 -MINLENE® -MAXLENE=200000000
-USRE=US09817198 @CGN 1 1 85 @runat_15032004 101743 20457 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NGG_SCORES=0 -MAXIT -DEPBLOKE=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THERADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 16, Appli
Sequence 16, Appli
Sequence 7, Appli
Sequence 646, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 10, Appli
Sequence 119, Appli
Sequence 126, Appli
Sequence 142, Appli
Sequence 142, Appli
Sequence 142, Appli
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1417.465 Million cell updates/sec
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                    nucleic search, using frame_plus_p2n model
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US-09-566-921-7
US-09-620-312D-646
US-09-18-184-2
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APPLICANT: Shah, Purvi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu 180
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Matches:
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Mismatches:
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Patent No. 6300472
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
                                                                                                                                                      6.68e-52
478.50
65.84%
45.05%
           SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
INFORMATION FOR SEQ ID NO:
                                                                                            LIBRARY: LIVRTUT04
CLONE: 2514506
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81 AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 AIGAACCCCGAATATGACTACCTGTTTAAGCTGCTTTTGATTGGCGACTCAGGCGTGGGC
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                               ZINCATANA COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/154,602
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-817-198C-2 (1-212) x US-09-154-602-4 (1-925)
                                                                                                                                                                                                                                                                                                                                                                           NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
ADDRESSONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,901
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
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478.50
65.84$
45.05$
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                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                  ADDRESSEE: Incyte Phar
STREET: 3174 Porter Dr
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
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                                                                                                                            USA
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141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
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GGCCAGATGGGCATCCTAGTTGTTCGAGACCAGCCCAAGGAGAATGTCAACGTGGAAGAG 558
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                          121 AsnLysAlaAspGluGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
                                                                                                                                                                                                             439 AATAAGAATGACGACCCTGAGCGGAAGGTGGTGGAGACGGAAGATGCCTACAAATTCGCC 498
                                                                                                                                                                                                                                                                                                                                          161 SerPheThrArgLeuThrGluLeuValleuGlnAlaHisArgLysGluLeuGluGlyLeu 180
                                                                                   101 LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DEAD PC COMPATIBLE
CORREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1422, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice AL-Young
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                ::: ::: | | | | :::::: | 619 CAGCAGCAACAACAACGATGTG 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1422:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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JAY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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US-09-016-434-1422
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IMMEDIATE SOURCE:
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APPLICANT: MCCLelland, Michael
APPLICANT: Terakke, Thomas
FAPLICANT: Terakke, Thomas
TITLE OF INVENTION: Using Same
TITLE OF INVENTION: Using Same
FILE REFERENCE: P-PH 3457
CURRENT FILING DATE: 1999-04-27
FRIOR APPLICATION NUMBER: 60/083,331
FRIOR APPLICATION NUMBER: 60/083,070
FRIOR APPLICATION NUMBER: 60/089,070
FRIOR APPLICATION NUMBER: 60/18,624
FRIOR APPLICATION NUMBER: 60/18,624
FRIOR APPLICATION NUMBER: 60/18,624
FRIOR APPLICATION NUMBER: 60/18,624
FRIOR PILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
                          591 GGAGCAGCCTCTGGGGGCGGCGGCCCAATCTCAAGATCGACACCACCCCTGTAAAGCCG 650
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                                                                                   141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
                                                                                                                                                                   161 SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu 180
                                                                                                                                                                                                                                                       181 ArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLysPro 200
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                                                                                                           ----ATGACCATGGCTGCTGAAATCAAAAGCGGATGGGGCCT
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Matches:
Conservative:
Mismatches:
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Patent No. 6495319
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477.50
72.34%
46.28%
43.21%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-300-958A-16
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Pred. No.:
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LENGTH: 730
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us-09-817-198c-2.rni

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121 AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
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                                                                                                                                                                                                                                                                41 ileGlyvalAspPherysMetLysThrileGluValAspGlyIleLysValArglleGln 60
                                                                                                                                                                                                                      81 AlaGlnGly1lePheLeuValTyrAepIleSerSerGluArgSerTyrGlnHis1leMet
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                                                                                                                                 1 MetalaLysGlnTyraspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyValGly
   and
                 Conservative:
Mismatches:
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TITLE OF INVENTION: No. 6569662el Nucleic Acids
TITLE OF INVENTION: Polypeptides
                                                                                                  US-09-817-198C-2 (1-212) x US-09-566-921-7 (1-8137
   Matches:
                                                   Indel8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REPERENCE: 784CIP28
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT APPLICATION NUMBER: 200-07-19
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 646, Application US/09620312D
Patent No. 656962
GENERAL INPORMATION:
APPLICANT Tang Y. Tom
APPLICANT Tang Y. Tom
APPLICANT Agundi, Vinod
APPLICANT Shang, Vine
APPLICANT Chen, Rui-hong
APPLICANT Chen, Rui-hong
APPLICANT Chen, Rui-hong
APPLICANT Xeo, Qing A.
APPLICANT Yang Yonghong
APPLICANT Yang, Yonghong
APPLICANT Yang, Yonghong
APPLICANT Yang, Yonghong
APPLICANT Zhou, Ping
APPLICANT Zhou, Ping
APPLICANT Mang, Jian-Rui
APPLICANT Mang, Jian-Rui
APPLICANT Mang, Jian-Rui
APPLICANT Mang, Jian-Rui
APPLICANT Mang, Jian-Rui
APPLICANT Mang, Jian-Rui
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Wang, Zhiwei
John Tillinghast
 467.00
72.84%
51.85%
42.26%
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               Percent Similarity:
Best Local Similarity:
Query Match:
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APPLICANT:
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                                                                                                                                                  1 MetAlaLysGlnTyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyValGly
                                                                                                                                                                                  60 Argaarcccgaarargarrarrarrarrcaagrracrrcrarrgscgacrcagggrand
                                                                                                                                                                                                               LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09566921
Fatent No. 6682888
GENERAL INFORMATION:
APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora W.
APPLICANT: Tingley, Debora W.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
FILE REFERENCE: PA-0024 US
CURRENT APPLICATION UNDERER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL PROGRAM
SEQ ID NO 7
LENGTH: 8137
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OTHER INFORMATION: Incyte ID No. 6682888 411474.10
NAME/KEY: unsure
LOCATION: 3488-3788
OTHER INFORMATION: a, t, c, g, or other
                  Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                  US-09-817-198C-2 (1-212) x US-09-016-434-1422 (1-723)
     Length:
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1.38e-50
467.00
72.84%
51.85%
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                                Percent Similarity:
Best Local Similarity:
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Pred. No.:
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Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION NUMBER: 09/488,725
         PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL FL genes Version 1.0
SEQ ID NO 646
LENGTH: 1069
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456.50
62.86%
39.52%
41.31%
                                                                                      TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (156)..(839)
US-09-620-312D-646
                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
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Mismatches:
Indels:
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TITLE OF INVENTION: NOVEL RAB PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSES: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
CITY: USA
ZID.
                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,873
FILING DATE: Filed Herewith
CLASSIFICATION: 435
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Matches:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCET DOCKET NUMBER: PF-0240
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1340 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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67.84%
45.23%
39.59%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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Sequence 2, Application US/08824873 Patent No. 584317 GENERAL INFORMATION: APPLICANT: Hillman, Jennifer L.

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US-09-075-454-10
; Sequence 10, Application US/09075454
; Patent No. 6391580
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Tang, Y. Tom
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aAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLysGluTy 143
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537 GGCTCCCAGCGAGCCGCGTTCCGGCTGCATTACGTTAAGAGGAGGATCGA 591
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Mismatches:
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Gaps:
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FastSEQ for Windows Version 2.0
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Patent No. 6010859

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Geogler, Karl
TITLE OF INVENTION: NOVEL RAB PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
STREET: 3174 Porter Drive
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CLASSIFICATION:
PRIASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/824,873
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BAILINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 9F-02/
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/09/198,184
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LENGTH: 1340 base pairs
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STRANDEDNESS: single
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                            501 AGCCATAGCA---
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SOFTWARE: FASTSEC
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CITY: Palo Alto
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143 rglyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheTh 163
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------AAGGAGTTGAAGCAGCGCTCCATGAA 536
                                                                                      163 rArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArgMetAr 183
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                                                          Leu-CysArgPheThrAspAsnGluPhe---HisSerSerHisIleSerThrIleGlyVa
                                                                                                                                                     43 lAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGlnIleTrpAs
                                                                                                                                                                            prhralaglyglngluargryrglnThrIleThrLysGlnTyrTyrargargalnGl
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3174 Porter Drive
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,454
PILING DATE: Herewith
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APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
APPLICANT: Batra, Sajeev
APPLICANT: Batra, Sajeev
TITLE OF INVENTION: Mariah R.
NUMBER OF SEQUENCES: 14
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APPLICATION NUMBER: 08/766,551
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APPLICANT
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Matches:
Conservative:
Mismatches:
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        ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0168-1 CIP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEX:
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 base pairs
TYPE: nucleic acid
STARNDEDNESS: single
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US-09-620-312D-959
; Sequence 959, Application US/09620312D
FILING DATE: DECEMBER 12, 1996
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429.00
68.48%
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579 GCCGGCCATCAG 590
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; CLONE: 1528559
US-09-075-454-10
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Best Local Similari
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103 TACGACCTCACGGGCAAGGTGATGCTTCTGGGAGACACAGGCGTCGGCAAAAACATGTTTC 162
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TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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Matches:
Conservative:
Mismatches:
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CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR PILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SEQ ID NO 959
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68.48%
44.57%
38.82%
         Tang, Y. Tom
Liu, Chenghua
Asundi, Vinod
Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Vare, Aidong J.
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John Tillinghast
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Wang, Jian-Rui
Zhou, Ping
Ma, Yunqing
Wang, Dunrui
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ORGANISM: Homo sapiens
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US-09-620-312D-959
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Best Local Similarity:
Query Match:
INFORMATION:
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NAME/KEY: CDS
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us-09-817-198c-2.rni

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124 AspGluGluGluLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLysGluTyr 143
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                    164 ArgieuThrGluieuValleuGlnAlaHisArgiysGluieuGluGlyLeuArgMetArg
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TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
TITLE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
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Mismatches:
Indels:
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Matches:
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GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
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SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 426
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40.49%
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John Tillinghast
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Ren, Feiyan
Chen, Rui-hong
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Wehrman, Tom
Xue, Aidong J.
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Wang, Jian-Rui
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
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Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-620-312D-426
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 raceaccrcaceccaaecrearecrrcreseaeacacacecercescaaacaretrc 150
                        144 GlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThr 163
                                                                                                                                               164 ArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArgMetArg 183
   124 AspGluGluGlnLysArgGlnValGlyArgGluGlnGlnGlnLeuAlaLysGluTyr 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThralaclyclncluargTyrclnThr1leThrLysclnTyrTyrargArgalaclnCly 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TyraspvalleuPheArgLeuLeuLeuIleGlyAspSerGlyValGlyLysThrCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 LeuCysArgPheThrAspAsnGluPheHisSer --- SerHisileSerThrIleGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 AspPheLysMetLysThrlleGluValAspGlyIleLysValArgIleGlnIleTrpAsp
                                                                                            FEATURE:
NAMEKKEY: misc feature
OTHER INFORMATION: Incyte ID No. 6426186 412477.1CB1
US-09-484-970B-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-817-198C-2 (1-212) x US-09-484-970B-142 (1-2612)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Jones, Karen A.
APPLICANT: JOHENTH, WAYNE
APPLICANT: Walker, Michael G.
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION UNMERE: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL Program
LENGTH: 2612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                :-09-484-970B-142
Sequence 142, Application US/09484970B
Patent No. 64264B
GENERAL INFORMATION:
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429.00
68.48%
44.57%
38.82%
                                                                                                                                                                                                                         184 AlaSerAsnGlu 187
                                                                                                                                                                                                                                               ||| :::::
610 GCCGGCATCAG 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
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AspileSerSerGluArgSerTyrGlnHisIleMetLysTrpValSerAspValAspGlu 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLysGluTyrGlyMetAspPheTyr 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThrArgLeuThrGluLeu 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgTyrGlnThrIleThrLysGlnTyrTyrArgArgAlaGlnGlyIlePheLeuValTyr 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 ArgleuleuleulleGlyAspSerGlyValGlyLysThrCysLeuleuCysArgPheThr 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 AspAsnGluPheHisSer---SerHisIleSerThrIleGlyValAspPheLysMetLys 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 ThrileGluValAspGlyIleLysValArgIleGlnIleTrpAspThrAlaGlyGlnGlu 68
                                                                                                                               LOCATION: (17)..(18)
OTHER INFORMATION: The n at positions 17 through 18 represents an OTHER INFORMATION: unknown.
                                                                             represents
                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (108)
OTHER INFORMATION: The n at position 108 represents an unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (204)

; OTHER INFORMATION: The n at position 204 represents an unknown.

US-09-255-920A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The n at position 138 represents an unknown
                                                                                                                                                                                                                                                                                                                                         The n at position 726 represents an unknown
                                                                                                                                                                                                                                                                                                                                                                                                 The n at position 823 represents an unknown
                                                                                                                                                                                                           LOCATION: (22)
OTHER INFORMATION: The n at position 22 represents an unknown
                                                                                                                                                                                                                                                             LOCATION: (25)
OTHER INFORMATION: The n at position 25 represents an unknown
                     OTHER INFORMATION: The n at position 12 represents an unknown
                                                    LOCATION: (14)...(15)
OTHER INFORMATION: The n at positions 14 through 15
OTHER INFORMATION: unknown.
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-817-198C-2 (1-212) x US-09-255-920A-6 (1-842)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
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63.24%
42.65%
38.37%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: ungure
LOCATION: (138)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                           LOCATION: (726)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
                                                                                                                                                                                         NAME/KEY: unsure
                                                                                                                                                                                                                                                NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
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                                                                                                                                                       CTGCTGGTGTACGACATTACAAGGCGTGAAACCTTCAACCACTGACCTCATGGTTAGAG 400
                                                                                                                                                                                                                                                                                                          461 CTAGAGTCCCGCAGGGATGTGAAGAGAAGAAGAAGAGGCCTTTGCTAGGGAGCATGGA 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||| :::||||||||||| crcacgacctcacagataaggaggagg 220
                                                                               125 GluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLysGluTyrGly 144
                                                                                                                                                                                                                                                                                                                                                                                                                                    145 MetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThrArg 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 LeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArgMetArgAla 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --------TTTGATGTCCACAATGAGGCAAATGGCATCAAGATTGGCCCCAA 664
                                                                                                                                                                                                         85 PheleuValTyrAspileSerSerGluArgSerTyrGlnHisIleMetLysTrpValSer 104
                                                                                                                                                                                                                                                                                   105 AspValAspGluTyrAlaProGluGlyValGlnLyslleLeuIleGlyAsnLysAlaAsp 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLysProGluGlyProAla 204
                                                          64
                                                                                                                               65 AlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArgAlaGlnGlyIle 84
                                                        PhelysMetLysThrlleGluValAspGlyIleLysValArglleGlnIleTrpAspThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (6)...(8)
OTHER INFORMATION: The n at positions 6 through 8 represents an OTHER INFORMATION: unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fisher, Joseph
APPLICANT: Lorens, James
APPLICANT: Lorens, James
APPLICANT: Lorens, James
APPLICANT: Lorens, James
APPLICANT: Lory Ying
APPLICANT: Luo, Ying
APPLICANT: Shen, Mary
TITLE OF INVENTION: Shen, Mary
TITLE OF INVENTION: A65905-1/D0B/RMS
CURRENT APPLICATION NUMBER: US/09/255,920A
CURRENT APPLICATION NUMBER: 60/075,534
PRIOR FILING DATE: 1998-02-23
PRIOR APPLICATION NUMBER: 60/086,650
PRIOR APPLICATION NUMBER: 60/086,650
PRIOR APPLICATION NUMBER: 1998-02-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 AsnSerSerLysThr 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              665 CAGTCAATTTCAACA 679
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OTHER INFORMATION: The
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LOCATION: (6)..(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS-09-255-920A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 6
LENGTH: 842
                                                                                                                                                                    281
                                                                                                                                                                                                                                              341
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547 AACGGCATCAAAATTGGCCCTCAGCATGCTACCAATGCATCTCACGGAGGCAACCAA 606
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                                                                                                                                                                                                                                                                                                                                                                                                                         105 AgpvalAspGluTyrAlaProGluGlyValGlnLysIleLeuileGlyAsnLysAlaAsp 124
                                                                                                                                                                                                                                                                   426
                                                                                                                                                                                                                                                                                                            145 MetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThrArg 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---GluGluGl 196
                                                       85 PheLeuValTyrAspileSerSerGluArgSerTyrGlnHisIleMetLysTrpValSer 104
                                                                                 ||| :::||||:::||| 367 TTAGAATCTAGGAGGAGGAAGGAGGAAGGTGAAGGTTTTGCACGAGGAGCATGGA
                                                                                                                                                                                                                                                                                                                                          165 LeuThrGluLeuVal-LeuGlnAlaHisArgLysGluLeuGluGlyLeuArgMetArg--
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Sequence 28, Application US/08888077A

Sequence 28, Application US/08888077A

Patent No. 6020143

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMENS, JOHANNA M
APPLICANT: RAJER, ADAL E

TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.
NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:
ADDRESSE: LERRIER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
STREET: 600 SOUTH AVENUE WEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CIP IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,077A
FILING DATE: 03-JUL-1997
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,541
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: PALISI, THOMBER: 36,629
REFERENCE/DOCKET NUMBER: 36,629
REFERENCE/DOCKET NUMBER: 36,629
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 -AlaSerAsnGluLeuAlaLeuAlaGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 uGluGlyLysProGluGlyProAla 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (908) 654-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (908) 654-7866
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 970 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 07090-1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                              189 AlaLeuAlaGluLeuGluGluGluGluGlyLysProGlu-GlyProAlaAsnSerSerLy 208
                                                                                                                                                      621
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    --GAGTTG 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 PhelysMetLysThrIleGluValAspGlyIleLysValArgIleGlnIleTrpAspThr 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 AlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArgAlaGlnGlyIle 84
                                                                                   574 GCCTTTCTGGCAATTGCCAAGGAA------CTGAAATACCGTGCAGGGAGGCAG---
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Rhodes, Kenneth
APPLICANT: Betry, Maria
APPLICANT: Ling, Huai-Ping
APPLICANT: Ling, Huai-Ping
APPLICANT: An, Wendian
TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
FILE REFERENCE: MNI-070CP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT PEPLICATION NUMBER: US/09/399,913
CURRENT PELING DATE: 1999-09-21
EARLIER APPLICATION NUMBER: USN 60/110,277
EARLIER APPLICATION NUMBER: USN 60/110,033
EARLIER APPLICATION NUMBER: USN 60/110,033
EARLIER FILING DATE: 1998-11-25
EARLIER FILING DATE: 1998-11-25
EARLIER FILING DATE: 1998-11-26
EARLIER FILING DATE: 1998-11-20
EARLIER FILING DATE: 1999-04-23
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NUMBER OF SEQ ID NOS: 73
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    538 GAGACCAGTGCCAAGACTGGCATGAACGTG
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-113 (793)
CURRENT APPLICATION NUMBER: US/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
SEQ ID NO 74
LENGTH: 1054
12 US-10-363-616-74 NPA
9 US-09-764-868-88 AB.
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15 US-09-764-868-507
15 US-10-264-04-290
14 US-10-084-817-256
9 US-09-925-300-631
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19 US-09-834-975-895
10 US-09-834-975-896
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14 US-10-128-714-7600
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; Publication No. US2004004181A1
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-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-G-cgnz 1/USFTO spool p/US09817198/runat_15032004_101745_20492/app_query.fasta_1.391
-G-cgnz 1/USFTO spool p/US09817198/runat_15032004_101745_20492/app_query.fasta_1.391
-DE-bublished Applications NA -OFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pct -NORM=ext -HEARBIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09817198 @CGN 1 1 333 @runat 15032004 101745_20492
-NCPU=c -ICPU=3 -NO MMAP -LARGEQUERY NEG SCORES=0 -WART -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGĀPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                     March 21, 2004, 08:59:39; Search time 311 Seconds (without alignments) 2521.609 Million cell updates/sec
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                                                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Perfect score:
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Database

Score

Result No.

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Patent No. US20020168711A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232

CURRENT APPLICATION NUMBER: US/09/764,868

CURRENT FILING DATE: 2001-01-77

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 1510

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 88

LENGTH: 2021
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                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Homo sapiens
                                              Percent Similarity:
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DB:
                   Alignment Scores:
Pred. No.:
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Sequence 1, Application US/09817198A

Sequence 1, Application US/09817198A

Patent No. US20020146758A1

GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001188

CURRENT APPLICATION NUMBER: US/09/817,198A

CURRENT FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 3257

TYPE: DNA
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Length:
Matches:
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Mismatches:
Indels:
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             FEATURE:
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Sequence 507, Application US/09764868

Sequence 507, Application US/09764868

BENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INFORMATION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PT23

CURRENT APPLICATION NUMBER: US/09/764,868

CURRENT APPLICATION NUMBER: US/09/764,868

CURRENT FILE CETING DATE: 2001-01-17

NUMBER OF SEQ ID NOS: 1510

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 507

LENGTH: 566

TYPE: DNA
                                                    Length:
Matches:
Conservative:
Mismatches:
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                                          1.91e-130
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100.00%
                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
; ORGANISM: Human
US-09-817-198A-1
                                        Alignment Scores:
Pred. No.:
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251 ATCTGGGACACTGCAGGGGAGGAGATACCAGACCATCACAAAGCAGTACTATCGGCGG 310
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PA133P1
CURRENT APPLICATION: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
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Matches:
Conservative:
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US-10-264-049-290
Sequence 290, Application US/10
Publication No. US20040005579A1
GENERAL INFORMATION:
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                                             LOCATION: (493)
OTHER INPORMATION: n
NAME/KEY: SITE
LOCATION: (538)
OTHER INPORMATION: n
NAME/KEY: SITE
LOCATION: (563)
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Best Local Similarity:
Query Match:
DB:
LOCATION: (484)
OTHER INFORMATION:
NAME/KEY: SITE
                                                                                                                                                                 OTHER INFORMATION:
US-09-764-868-507
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142 GluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSer 161
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 82 GlnGly1lePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMetLys 101
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                                                                    102 TrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGlyAsn
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OTHER INFORMATION: Incyte ID No. US20030119009A1 4004223CB1
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APPLICANT: Sharon E. Plon
APPLICANT: Sharon E. Plon
APPLICANT: Jason M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
FILE REPERENCE: PA-0046 US
CURRENT APPLICATION NUMBER: US/10/084,817
CURRENT FILING DATE: 2002-25
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Matches:
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Publication No. US20030119009A1
GENERAL INFORMATION:
APPLICANT: Susan Stuart
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PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SOFTWARE: PERL Program
SEQ ID NO 256
LENGTH: 995
                                                                                                                                                                                                                                                                                                                                            182 MetArgAlaSerAsnGlu 187
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US-10-084-817-256
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ORGANISM: Homo sapiens
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Best Local Similarity:
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LOCATION: 960
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Query Match:
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Matches:
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LOCATION: (2357)..(2357)
OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (2309)..(2309)
OTHER INFORMATION: n equals a,t,g, or c
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              PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ 1D NOS: 4360
SOFTWARE: Patentin Ver. 3.1
SEQ 1D NO 290
LENGTH: 2411
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OTHER INFORMATION: n equals a,t,g, or
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LOCATION: (21)...(21)
OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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76.88%
52.69%
FILING DATE: 2001-06-07
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (5)...(5)
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LOCATION: (2293)..(229
                                                                                                                                    ORGANISM: Homo sapiens
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Best Local Similarity:
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                                                                                                                      TYPE: DNA
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141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
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GCTTTTAGTTCCCTGGCCCGGGACATCTTGCTCAAGTCAGGAGGCCGGAGATCAGGAAAC
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patent No. US20020151681A1

GENERAL INFORMATION:

APPLICANT: Craig Rosen,

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA101

CURRENT APPLICATION NUMBER: US/09/925,300

CURRENT APPLICATION NUMBER: DCT/US00/05988

PRIOR APPLICATION NUMBER: PCT/US00/05988

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 631

LENGTHAN: 1537
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                                                               US-09-817-198C-2 (1-212) x US-09-925-302-91 (1-1274)
   Gaps:
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ORGANISM: Homo sapiens
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                                                                                                 AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlnGlnLeuAla 140
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247 ATCGGAATTGATTTCAAGATCCGCACTGTGGATATAGAGGGGAAGAAGATCAAACTACAA 306
                                                            61 IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
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Fatent No. US20020044941A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
FRIOR PELING DATE: 2000-03-08
FRIOR PILING DATE: 2000-03-08
FRIOR PILING DATE: 1999-03-12
FRIOR APPLICATION NUMBER: 60/124,270
FRIOR APPLICATION NUMBER: 60/124,270
FRIOR PILING DATE: 1999-03-12
SOFTWARE: PATENTIN Ver. 2.0
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; OTHER INFORMATION: n equals a,t,g,
US-09-925-302-91
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NAME/KEY: misc feature
LOCATION: (1268)
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NAME/KEY: misc feature
LOCATION: (1264)
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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LENGTH: 1274
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Pred. No.:
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; Sequence 9, Application US/09794257; Patent No. US20020009804A1; GENERAL INFORMATION:
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528.50
80.68%
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                                                           530.50
82.56%
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48.01%
                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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ORGANISM: homo
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Pred. No.:
                             Alignment Scores:
Pred. No.:
JS-10-096-534-38
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US-10-096-534-38

US-10-096-534-38

Sequence 38, Application US/10096534

Publication No. US20030166887A1

GENERAL INFORMATION:

APPLICANT: The Brigan and Women's Hospital, Inc.

APPLICANT: Wizuno, Shuichi

APPLICANT: Mizuno, Shuichi

APPLICANT: Mizuno, Shuichi

APPLICANT: Mizuno, Shuichi

APPLICANT: US/10/096,534

CURRENT APPLICATION NUMBER: US/10/096,534

CURRENT APPLICATION NUMBER: US 60/274,980

PRIOR APPLICATION NUMBER: US 60/274,980

PRIOR FILING DATE: 2001-03-12

NUMBER OF SEQ ID NOS: 79

SOFTWARE: Patentin version 3.0

SEQ ID NO 38

LENGENT: 3164

TYPE: DNA

CREATIONS

CREATIONS

CREATIONS

CREATIONS

CREATIONS

CREATIONS

CONDITIONS

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                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                 O
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                            ; LOCATION: (5)
; OTHER INFORMATION: n equals a,t,g,
US-09-925-300-631
                                                                                                          1.75e-57
530.50
82.56%
55.81%
   FEATURE:
NAME/KEY: misc feature
                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                gnment Scores:
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APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 32705, 23224, 27423, 32700, 32712, No. US20020009804A1e1
TITLE OF INVENTION: Human G-Proteins
FILE REPERENCE: 35800/209285
GURRENT APPLICATION WUMBER: US/09/794,257
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 60/185,606
PRIOR APPLICATION NUMBER: 60/185,606
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FRASESQ for Windows Version 4.0
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Fatent No. US20020009804A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 32705, 23224, 27423, 32700, 32712, No. US20020009804A1e1
TITLE OF INVENTION: Human G-Proteins
TITLE OF INVENTION: Human G-Proteins
FILE REPRENCE: 35800/209288
CURRENT APPLICATION NUMBER: US/09/794,257
CURRENT FILING DATE: 2001-02-27
FRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FRSESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                      81 AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
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                                                      US-09-817-198C-2 (1-212) x US-09-794-257-9 (1-624)
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47.83%
 Best Local Similarity: 53.98%
Query Match: 47.83%
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US-09-794-257-7
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APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrew
APPLICANT: Bolt, Andrew
APPLICANT: Wan Huffel, Christophe
TITLE OF INVENTION: POR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: POR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: POR UNAN CANCERS
FILE REFERENCE: MRI-016B
CURRENT PELLING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOPTWARE: FRESEEQ for Windows Version 4.0
SEQ ID NO 879
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                                      MetalaLysGlnTyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyValGly
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US-09-817-198C-2 (1-212) x US-09-794-257-7 (1-1161)
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OTHER INFORMATION: n = A,T,C or
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Sequence 894, Application US/09834975
; Sequence 894, Application US/09834975
; Batent No. US20020110815A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Brown, Jeffrey
; APPLICANT: Bolt, Andrew
; TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION:
; TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION:
; TITLE OF INVENTION: FOR THE IDENTIFICATION, AND THERAPY
; TITLE OF INVENTION: GOF HUMAN CANCERS
; TITLE OF INVENTION: GOF HUMAN CANCERS
; TITLE OF INVENTION: GO/197,538
; FILE REFERENCE: MRI-0168
; CURRENT APPLICATION NUMBER: 60/197,538
; PRIOR PLILOADIS: 2000-04-14
; NUMBER OF SEQ ID NOS: 1046
; SEQ ID NO 894
; LENGTH: 2497
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OTHER INFORMATION: n = A,T,C or
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ORGANISM: Homo sapiens
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Sequence 885, Application US/09834975
Patent No. US20020110815A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrew
APPLICANT: Bolt, Andrew
TITLE OF INVENTION: FOR THE IDENTIFICATION ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION: OF HUMAN CANCERS
CURRENT FILING DATE: 2001-04-13
PRIOR PILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 885
LENGTH: 2497
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                                                           US-09-817-198C-2 (1-212) x US-09-834-975-879 (1-2497)
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ORGANISM: Homo sapiens
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Sequence 896, Application US/09834975

Sequence 896, Application US/09834975

Patent No. US20020110815A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Bolt, Andrew

APPLICANT: Bolt, Andrew

APPLICANT: Van Huffel, Christophe

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS

TITLE OF INVENTION: POR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY

TITLE OF INVENTION: OF HUMAN CANCERS

TITLE REPRESENCE: MRI-016B

CURRENT APPLICATION NUMBER: US/09/834,975

CURRENT FILING DATE: 2001-04-13

PRIOR PILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 1046

SOCTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 896

LENGTH: 2497
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; OTHER INFORMATION: n = A,T,C or G
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 15, 2004, 11:12:58; Search time 20 Seconds (without alignments) 1019.630 Million cell updates/sec

US-09-817-198C-2 1105 1 MAKQYDVLFRLLLIGDSGVG......LEBEBGKFBGPANSSKTCWC 212

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%			SOMMENTES	
Result No.	Score	Query Match	Query Match Length	DB	QI	Description
!	1077	97.5	212	~	F42148	GTP-binding protei
7	559	50.6	224	~	T33855	hypothetical prote
c	545	49.3	207	~	B49647	GTP-binding protei
4	545	49.3	207	7	B36364	
S	532	48.1	203	~	A49647	
9	531.5	48.1	200	7	A38625	
7	530.5	48.0	200	7	D36364	
80	530	48.0	209	8	B38625	
9	526	47.6	206	7	178851	GTP-binding protei
10	522.5	47.3	200	~	B42148	
11	519	47.0	216	7	T45901	GTPase Atrabs - Ar
12	514	46.5	201	~	T28971	hypothetical prote
13	512	46.3	216	~	833900	124
14	512	46.3	216	~	T48378	
15	510	46.2	200	7	S12790	
16	509	46.1	215	N	T14565	
17	508.5	46.0	215	~	S57478	
18	508	46.0	216	7	JS0640	
19	507.5	45.9	222	N	T14405	
20	206	45.8	216	7	S57471	
21	505.5	45.7	217	~	836365	
22	502.5	45.5	215	7	857462	
23	501	45.3	203	~	S51495	
24	495.5	44.8	204	~	JC7589	O
25	492.5	44.6	215	~	S57474	ŭ
56	483.5	43.8	208	N	A34716	
27	483	43.7	208	7	A38202	
28	482	43.6	203	7	S34253	
59	480	43.4	202	7	S38740	
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B34716 S72515 JC2488 JC24105 JC4105 JC4337 S41430 B86153 JC1247 S3096 F133781 F14391 F14391 F14391 F18242 F38339 TVRYQP	ALIGNMENTS	otein rab15 - rat tus norvegicus (Norway rat) 42148 A.; Anzai, K.; Scheller, R.H. 267, 5768-5775, 1992 A novel low molecular weight GTP- 42148 mber: A42148; MUD:92210533; PMID:1 42148 122 * CELP- 11 poptotein; nuclectide P binding; lipoptotein; nuclectide P tanalarion elongation factor Tu : translation elongation factor Tu : translation elongation factor Tu : translation elongation factor Tu : muclectide-binding motif A (P-loo on: GTP-binding NXCD motif ing site: geranyl-geranyl (Cys) (co gy.5%; Score 1077; DB imilarity 97.6%; Pred. No. 1.2e- Conservative 2; Mismatches MAKOYDVLFRILLIGDSGVGKTCLLCRFTDNEFHS MAKOYDVLFRILLIGDSGVGKTCLLCRFTDNEFHS NKADEEQKROVGREGGOLAKEYGMDFYETSACTN	norhabd sion 29 , Novem
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0 11 12 14 14 14 14 14 14 14 14 14 14 14 14 14		RESULT 1 F42148 GTP-binding protein rab15 - ra C;Speciaes: Rattus norvegicus (C;Speciaes: Rattus norvegicus (C;Accession: F42148 R;Elferink, L.A.; Anzai, K.; S J; Biol. Chem. 267, 5768-5775, A;Title: rab15, a novel low mo A;Reference number: A42148; MU A;Recession: F42148 mu A;Recession: P42148 mu A;Recession: RP3-124 mu A;Region: GTP-binding; Lipop F;9-124/Region: nucleotide-bin F;15-22/Region: nucleotide-bin F;15-22/Region: nucleotide-bin F;15-22/Region: mucleotide-bin F;15-22/Region: mucleotide-bin F;15-22/Region: mucleotide-bin F;10,212/Binding site: gerany Cuery Match Best Local Similarity 97.6 matches 207; Conservative O; Ma	RESULT 2 T33855 hypothetical protein C; Species: Caenorhabd C; Date: 29-Oct-1999 # C; Accession: T33855 R; Ledwith, J; Biewal submitted to the EMBL A; Description: The se

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GTP-binding protein Rab13 - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 02-Feb-2001 C; Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 02-Feb-2001 S; Louvarc C; Accession: A.9; Joberty, G.; Arpin, M.; Fontaine, J.J.; Hellio, R.; Tavitian, A.; Louvarc J. Cell Biol. 124, 101-115, 1994 A; Title: A small rab GTPase is distributed in cytoplasmic vesicles in non polarized cells A; Reference number: A49647; MUID:94124602; PMID:8294494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-207 < CHA>
A; Residues: 1-207 < CHA>
A; Cross-references: GB:X56385; NID:g920; PIDN:CABS6776.1; PID:g6006436
A; Cross-references: GB:X56385; NID:g920; PIDN:CABS6776.1; PID:g6006436
C; Superfamily: ras transforming protein; translation elongation factor Tu homology
C; Keywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop; F
F; P-22/Region: translation elongation factor Tu homology < BTU>
F; P-22/Region: GTP-binding motif A (P-loop)
F; P: 1-124/Region: GTP-binding NAXD motif
F; P: 1-153/Region: GTP-binding SAX/L motif
F; 204/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Canis lupus familiaris (dog)
C;Accession: 85364; Bsequence_revision 28-Mar-1991 #text_change 02-Feb-2001
C;Accession: 85364; B5564
R;Chavrier, P.; Vingron, M.; Sander, C.; Simons, K.; Zerial, M.
Mol. Cell. Biol. 10, 6578-6585, 1990
A;Title: Molecular cloning of YPTI/6BC4-related CDNAs from an epithelial cell line. A;Reference number: A36364; MUID:91061765; PMID:2123294
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A,Molecule type: mRNA
A,Residues: 1-203 <ZANA.
A,Cross-references: EMBL:X75593; NID:g452319; PIDN:CAA53266.1; PID:g452320
C,Superfamily: ras transforming protein; translation elongation factor Tu homology
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                                    61 IWDTAGQERFRITTAYYRGAMGIMLVYDITNEKSFDNIRNWIRNIEBHASADVEKMILG 120
                                                                                                                            121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
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les 99; Conservative 4
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A;Title: A small rab GTPase is distributed in cytoplasmic vesicles in non polarized cell A;Reference number: A49647; MUID:94124602; PMID:8294494
A;Accession: B49647
A;Status: nucleic acid sequence not shown
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A; Residues: 175-186 < 0.09s.

A; Residues: 175-186 < 0.09s.

C; Superfamily: ras transforming protein; translation elongation factor Tu homology

C; Keywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop;

E; 9-124/Domain: translation elongation factor Tu homology < ETU>

F; 15-22/Region: uncleotide-binding metif A (P-loop)

F; 15-1124/Region: GTP-binding NKXD motif

F; 151-153/Region: GTP-binding SAK/L motif

F; 204/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                A,Map position: 1
A;Introns: 10/3; 62/2; 82/3; 181/1
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
                                                                                                                                                          A;Cross-references: EMBL;AF106592; PIDN;AAC78494.1; GSPDB;GN00019; CESP:D1037.4
A;Experimental source: strain Bristol N2; clone D1037.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNINIKESFTRLTELVLQAHRKELEGL 180
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A; Molecule type: mRNA
A; Residues: 1-207 < 2AH>
A; Cross-references: EMBL:X56741; NID:g452317; PIDN:CAA40065.1; PID:g452318
A; Jöberty, G.; Tavitian, A.; Zahraoui, A.
R; Jöberty, G.; Tavitian, A.; Zahraoui, A.
A; Tille: Isoprenylation of Rab proteins possessing a C-terminal Caax motif.
A; Reference number: S36817; MUID:93387463; PMID:8375503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-May-1994 #text_change 19-Jan-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 50.6%; Score 559; DB 2; Best Local Similarity 55.3%; Pred. No. 2.4e-37; Matches 105; Conservative 42; Mismatches 39.
                   A;Accession: T33855
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Species: Homo sapiens (man)
C,Date: 03-May-1994 #sequence_revision
C,Accession: B49647; S36817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTP-binding protein rab8 - human
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   A;Reference number: Z21424
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                                                                                                                               A;Residues: 1-224 <LED>
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                                                                                                                                                                                                                        C;Genetics:
A;Gene: CESP:D1037.4
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Best Local S
Matches 99
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C, Superfamily: ras transforming protein; translation elongation factor Tu homology C, Keywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop; F;9-124/Domain: translation elongation factor Tu homology «ETU»
F;15-22/Region: nucleotide-binding motif A (P-loop)
F;151-124/Region: GTP-binding NIXD motif F;150-152/Region: GTP-binding SAK/L motif F;150-152/Region: GTP-binding SAK/L motif F;206/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                           Tu homology
binding; P-loop; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Discopyge ommata
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 02-Feb-2001
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 02-Feb-2001
C;Accession: B18625
A;Fitle: A family of ras-like GPP-binding proteins expressed in electromotor neurons.
A;Reference number: A38625; MUD:91115900; PMID:1899244
A;Status: preliminary
                            Richavrier, P.; Vingron, M.; Sander, C.; Simons, K.; Zerial, M.
Mol. Cell. Biol. 10, 6578-6585, 1990
A;Title: Molecular cloning of YPTI/SEC4-related cDNAs from an epithelial cell line.
A;Recence number: A36364; MUID:91061765; PMID:2123294
A;Accession: D36564
A;Status: preliminary
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A; Molecule type: mRNÅ
A; Residues: 1-200 c-CHA>
A; Residues: 1-200 c-CHA>
A; Cross-references: GB.X56387; NID:g914; PIDN:CAA39798.1; PID:g915
C; Superfamily: ras transforming protein; translation elongation factor Tu ho; Superfamily: ras translation protein; membrane trafflicking; nucleotide bind: F; 10-125, Domain: translation elongation factor Tu homology cETU>
F; 16-23/Region: nucleotide-binding motif A (P-loop)
F; 122-125/Region: GTP-binding SAK/L motif
F; 152-154 (Region: GTP-binding SAK/L motif
F; 152-154 (Region: GTP-binding SAK/L motif
F; 199, 200/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.0%; Score 530.5; DB 2; 55.8%; Pred. No. 3.8e-35; iive 46; Mismatches 29;
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Conservative 56; Mismatches
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Matches 96; Conservative
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        C; Accession: D36364; S15601
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99; Conserv
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A: Residues: 1-209 <NGS>
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                                                                                                                                         Lys, Asp, Ser) #sta
     nucleotide binding; P-loop;
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R;Agee, J.K.; Elferink, L.A.; Scheller, R.H.
Biol. Chem. 266, 2675-2680, 1991
A;Title: A family of ras-like GTP-binding proteins expressed in electromotor neurons.
A;Reference number: A38625; MUID:91115900; PMID:1899244
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C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; membrane trafficking; nucleotide binding; P-loop
F;10-125/Domain: translation elongation factor Tu homology <ETU>
F;16-23/Region: nucleotide-binding motif A (P-loop)
F;12-125/Region: GTP-binding NXXD motif
F;152-154/Region: GTP-binding SAK/L motif
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GTP-binding protein rab10 - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Discopyge ommata
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 02-Feb-2001
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                                                                                                                                                                                                                                                                              18; Gaps
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                                                                                                                                         Thr, Thr, Asn,
predicted
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                                                                                                                                                                                                                        2; Length 203;
C, Keywords: GTP binding, lipoprotein; membrane trafficking; nucl
F,9-124/Domain: translation elongation factor Tu homology <ETU>
F;15-22/Region: nucleotide-binding motif A (P-loop)
F;121-124/Region: GTP-binding NKXD motif
F;151-153/Region: GTP-binding SK/L motif
F;21,22,40,121,122,124,151/Binding site: Mg-GTP (Lys, Thr, Thr, F;200/Binding site: farnesyl (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                           43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Discopyge ommata)
                                                                                                                                                                                                                     48.1%; Score 532; DB 2
47.6%; Pred. No. 3e-35;
rative 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RMRASNELALAELEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRRSGN-----GNKP--PSTDLKTC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              electric ray
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                                                                                                                                                                                                                     Query Match
Best Local Similarity 47.6
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTP-binding protein oral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-200 <NGS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A38625
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Matches
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C;Accession: T45901
R;Blocker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aintrons: 25/1; 49/2; 83/1; 105/1; 137/3; 158/3; 189/3
A;Note: F4912.310
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
F;16-131/Domain: translation elongation factor Tu homology <FTU>
                                      ï
                                                                                                                                                                                                                        60 OIWDTAGOERYOTITKOYYRRAQGIFLVYDISSERSYOHIMKWVSDVDEYAPEGVQKILLI 119
                                                                                                                                                                                                                                                     61 QIWDTAGGERFHTITTSYYRGAMGIMLVYDITNGKSFENISKWLRNIDEHANEDVERMLL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 AGQERFRITTAAYYRGAMGILLVYDVTDESSFNNIRNWIRNIEQHASDSVNKILVGNKAD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 -EEQKRQVGREQGQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQA-----HRKELE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T2891
R;Wamsley, P.; Bradshaw, H.
R;Wamsley, P.; Bradshaw, H.
R;Wamsley, P.; Bradshaw, H.
R;Wamsley, P.; Bradshaw, H.
R;Wamsley, P.; Bradshaw, H.
R;Wamsley, P.; Bradshaw, H.
R;Wamsley, P.; Bradshaw, H.
R;Wamsley, P.; Bradshaw, H.
R;Wamsley, P.; Bradshaw, H.
R;Wamsley, P.; Bradshaw, H.
R;Wamsley, P.; Bradshaw, H.
R;Wamsley, P.; Bradshaw, H.
R;Description: The sequence of C. elegans cosmid T23H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: protein F4P12.310
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Sep-2000
                                                                                                                          12 YDYLIKLLIGDSGVGKSCLLRRFSDGSFTTSFITTIGIDFKIRTIELDGKRIKLQIMDT
                                                                                          1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
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; Pred. No. 1.7e-34;
46; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Accession: T45901
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-216 <BLO>
A;Cross-references: EMBL:AL132966
A;Experimental source: cultivar Columbia; BAC clone F4P12
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: T28971
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTPase AtRAB8 - Arabidopsis thaliana
55.2%;
Best Local Similarity 55.2%
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 51.9
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192 TIKINQSDQ 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 3
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Matches
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 02-Feb-2001
C;Accession: B42148
R;Elferink, L.A.; Anzai, K.; Scheller, R.H.
J. Biol. Chem. 267, 5768-5775, 1992
A;Title: rabl5, a novel low molecular weight GTP-binding protein specifically expressed A;Reference number: A42148; MUID:92210533; PMID:1313420
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: MEL
A;Gene: MEL
A;Gene: MEL
S;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; lipoprotein; nuclectide binding; P-loop; prenylated cysteine
F;9-124/Domain: translation elongation factor Tu homology <ETU>
F;12-124/Region: nucleotide-binding mociff A (P-loop)
F;121-124/Region: GTP-binding NAK/L mocif
F;151-153/Region: GTP-binding SAK/L mocif
F;203/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
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F;122-125/Region: GTP-binding NXXD motif F;152-154/Region: GTP-binding SAK/L motif F;199,200/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                              К.С.
                                                                                                                                                                                                                                                                                                            C;Species: Mus sp. (mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Feb-2001
C;Accession: I78851
R;Nimmo, E.R.; Sanders, P.G.; Padua, R.A.; Hughes, D.; Williamson, R.; Johnson, Oncogene 6, 1347-1351, 1991
Oncogene 6, 1347-1351, 1991
A;Title: The MEL gene: a new member of the RAB/YPT class of RAS-related genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 IWDTAGQERFRIITAYYRGAMGIMLVYDITNEKSFDNIRNWIRNIEBHASADVEKNILG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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A,Molecule type: mRNA
A,Residues: 1-206 <RES>
A,Cross-references: GB:S53270; NID:g234747; PIDN:AAB19682.1; PID:g234748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: 158355; MUID: 91360267; PMID: 1886711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.6%; Score 526; DB 2; 56.4%; Pred. No. 9.1e-35; ative 41; Mismatches 31;
                                   181 RMRASNELALAE-LEEEGKPEGPANSSK 208
                                                                       ----NENSLQEAVDKLKSPPKKPSQKKK 200
                                                                                                                                                                                                                                                     GTP-binding protein MEL - mouse N;Alternate names: gene MEL protein C;Species: Mus sp. (mouse)
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tes 93; Conservative
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Residues: 1-200 <ELF>
Cross-references: GB:M83677
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Matches

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GTP-linding protein ypt2 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 02-Feb-2001
C;Accession: S12790; S10493; T39214
R;Haubruck, H.; Engelke, U.; Mertins, P.; Gallwitz, D.
EMBO J. 9; 1957-1962, 1990
A;Title: Structural and functional analysis of ypt2, an essential ras-related gene in the A;Reference number: S12790; MUID:90269232; PMID:2112089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-200 <FRM>
A; Residues: 1-200 <FRM>
A; Cross - references: EMBL: X52864; NID: 95149; PIDN: CAA37045.1; PID: 95150
R; McDougall, R.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
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A;Residues: 1-200 <HAU>
A;Residues: references: BBL:X52469; NID:g5143; PIDN:CAA36707.1; PID:g5144
R;Pawell, E.; Hook, S.; Sweet, D.; Armstrong, J.
Nucleic Acids Res. 18, 4264, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: T39214
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                           A;Reference number: Z24492
A;Accession: T48378
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-216 <BEV>
                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
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C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Reywords: GTP binding; membrane protein; nucleotide binding; P-loop
F;16-131/Domain: translation elongation factor Tu homology <ETU>
F;12-292/Region: nucleotide-binding motif A (P-loop)
F;128-131/Region: GTP-binding NKXD motif
F;159-161/Region: GTP-binding SAK/L motif
                                                                                                                                          A,Map position: 1
A,Inkrons: 43/1; 147/2; 173/3
C,Superfamily: ras transforming protein; translation elongation factor Tu homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 QIWDTAGQERFHTITTSYYRGAMGIMLVYDITNAKSFDNIAKWLRNIDEHASEDVVKMIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 GNKADEEQKRQVGREQGQQLAKEYGNDFYETSACTNLNIKESFTRLTELVLQAHRKELEG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
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                     A,Cross-references: EMBL:U80033; PIDN:AAC48200.1; GSPDB:GN00019; CESP:T23H2.5
A,Experimental source: strain Bristol N2; clone T23H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Title: The patterns of gene expression in the tomato shoot apical meristem. A,Reference number: S33899; MUID:9322691; PMID:8467223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Incopersion esculentum (tomato)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 02-Feb-2001
C;Accession: 833900; 00233
R;Fleming, A.J.; Mandel, T; Roth, I.; Kuhlemeier, C.
Plant Cell 5, 297-309, 1993
A;Title: The patterns of gene expression in the tomato shoot apical merister
                                                                                                                                                                                                                                                                                                                                                                                                                      1 MARRPYDMLFKLLLIGDSGVGKTCLLYRFSDDAFNTTFISTIGIDFKIKTIELKGKKIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                                                                                                                                                            46.5%; Score 514; DB 2; Length 201;
ilarity 46.9%; Pred. No. 8e-34;
Conservative 48; Mismatches 51; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Indels 12; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKMPDSTD----EQSRDTVNPVQPQRQSSGGC 200
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EPQSIRINQSDQAGTA 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTP-binding protein ypt2 - tomato
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 100; Conserv
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Best Local Similarity
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A; Residues: 1-216 <FL2>
A; Residues: 1-201 < WAM>
                                                                                                                     A; Gene: CESP: T23H2.5
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N.Alternate names: protein F12E4.300
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C;Accession: T48378
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; submitted to the Protein Sequence Database, March 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: ras transforming protein; translation elongation factor Tu homology F;16-131/Domain: translation elongation factor Tu homology <FTU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 -BEOKROVGREOGOQLAKEYGMDFYETSACTNLNIKESF-----TRLTELVLQAHRK 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
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                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: EMBL:AL162751
A,Experimental source: cultivar Columbia, BAC clone F12E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 5
A;Introns: 25/1; 49/2; 83/1; 105/1; 137/3; 158/3; 189/3
A;Note: F12E4.300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.3%; Score 512; DB 2;
49.8%; Pred. No. 1.3e-33;
tive 43; Mismatches 46;
GTP-binding protein-like - Arabidopsis thaliana
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189 EPQGIKITKQDTAASSSTAEK 209
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Matches 100; Conservative
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A; Residues: 1-200 <MCD>

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A, Decovery Types.

A, Map position: 1

C; Superfamily: ras transforming protein; translation elongation factor Tu homology
C; Keywords: GTP binding; lipoprotein; membrane trafficking; mucleotide binding; P-loop;
F; 10-125/Domain: translation elongation factor Tu homology <ETU>
F; 16-23/Region: nucleotide-binding motif A (P-loop)
F; 122-125/Region: GTP-binding NKXD motif
F; 152-154/Region: GTP-binding SAK/L motif
F; 199, 200/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
, Cross-references: EMBL: Z99262; PIDN: CAB16405.1; GSPDB: GN00066; SPDB: SPAC9E9.07c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KOYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIW 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

46.2%; Score 510; DB 2; Length, 200;
Best Local Similarity 51.9%; Pred. No. 1.6e-33;
Matches 97; Conservative 39; Mismatches 43; Indels
                                                                                                    Genetics:
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4 KSYDYLIKLLLIGDSGVGKSCLLLRFSEDSFTPSFITTIGIDFKIRTIELDGKRIKLQIW 63

6 8 6

Search completed: March 15, 2004, 11:16:52 Job time : 21 secs

183 RASNELA 189 | | | : 176 DAENEFS 182

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

March 15, 2004, 11:09:18; Search time 18 Seconds (without alignments) 613.271 Million cell updates/sec

Title: Perfect score:

US-09-817-198C-2 1105 1 MAKQYDVLFRLLLIGDSGVG......LEEEEGKPEGPANSSKTCWC 212 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	15 HU	RB15 MOUSE	RB15_RAT	RABS HUMAN	RAB8 DISOM	RB13_HUMAN	RB10_DISOM	RB10_CANFA	RB10_HUMAN	RB8B_HUMAN	RB8B_RAT	RAB8_MOUSE	1 1	RAB1 BETVU	ARA3_ARATH	YPT2 VOLCA	RB10 RAT		SAS1_DICDI	YPT1_MAIZE	RIC1_ORYSA	SAS2_DICDI	RB1B_HUMAN	RB35_HUMAN		YPT1_PHYIN	ARAS ARATH				YPT2_MAIZE		RB1B_RAT
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Q05974 lymnaea sta P05711 rattus norv	P11620 schizosacch P11476 homo sapien P22125 discopyge o	P01123 saccharomyc Q96e17 homo sapien Q63482 mus musculu	Q9ulw5 homo sapien P51156 rattus norv P25228 drosophila	095716 homo sapien
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RAB1_LYMST RB1A_RAT	YPT1_SCHPO RB1A_HUMAN RAB1_DISOM	YPT1_YEAST RB3C_HUMAN RB3C_MOUSE	RB26 HUMAN RB26 RAT RAB3 DROME	RB3D_HUMAN
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205	203 205 202	206 227 227	190	219
42.4 42.4	42.3 42.3	41.3 41.3 51.2	41.0	40.2
469 468	467 467 464	456.5 456.5 455.5	454.5 452.5 449.5	444.5
34 35	36 37 38	39 410	4 4 4 4 2 4 4 4 4	45

ALIGNMENTS

115	THE FUNDAN STANDARD; PRT; 212 AA. FB15 HUWAN STANDARD; PRT; 212 AA. F89596; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 41, Last sequence update) Ras-related protein Rab-15. RAB15. RAB16. RAB1
	RESULUID DAY CON CONTRACTOR CONTR

synaptic vesicle membrane flow within the nerve terminal (By similarity). Similarity). Selongs to the small GTPase superfamily. Rab family.

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EMBL; AL139022; -; NOT ANNOTATED_CDS. Genew; HGNC:20150; RABIS. InterPro; IPR003579; GTPRASE Rab. InterPro; IPR003577; GTPRASE_RAS. InterPro; IPR003578; GTPASE_RAS. InterPro; IPR002041; RAN.

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212
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MEDLINE=22888257; PubMed=12477932;
A strausberg R.L. Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A lischul S.F. Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diatchento L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramoon R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
A Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Butcerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1105; DB 1; Length 212; 100.0%; Pred. No. 5e-81; Ative 0; Mismatches 0; Indels 0
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
S-geranylgeranyl cysteine
(By similarity).
S-geranylgeranyl cysteine
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D16A0C71797ED782 CRC64;
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28-FRB-2003 (Rel. 41, Last sequence update)
20-CCT-2003 (Rel. 42, Last annotation update)
Ras-related protein Rab-15.
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Matches 212; Conservative
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Q8K386;
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TD RELS_MC
DT 28-FEB.
DT 28-FEB.
DT 10-CFB.
GN RABLIS.
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CO MAMMALIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAKQYDVLFRILLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIDVDGIKVRIQ 60
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"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. C. Natl. Acad: Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: May act in concert with RAB3A in regulating aspects of synaptic yesicle membrane flow within the nerve terminal (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                    similarity).
-!- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.6%; Score 1090; DB 1; Length 212; 98.1%; Pred. No. 7.9e-80; ive 3; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTP-binding; Lipoprotein; Prenylation; Protein transport.
NP BIND 15 22 GTP (BY SIMILARITY).
NP BIND 63 67 GTP (BY SIMILARITY).
NP BIND 121 124 GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
S-geranylgeranyl cysteine
(By similarity).
S-geranylgeranyl cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y similarity).
ESC492846DD47F12 CRC64;
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01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
RAB15.
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INCEPPO; IPR003579; GTP@ase Rab.
INCEPPO; IPR003579; GTP@ase_Rab.
INCEPPO; IPR003578; GTP@ase_Rab.
INCEPPO; IPR003578; GTP@ase_Rho.
INCEPPO; IPR001801; RAN.
INCEPPO; IPR001801; RAN.
INCEPPO; IPR001801; RAN.
PRINTS; PR00171; ras; 1.
PRINTS; PR00171; ras; 1.
SWART; SW00175; RAB; 1.
SWART; SW00175; RAN; 1.
SWART; SW00177; RAN; 1.
SWART; SW00174; RAN; 1.
SWART; SW00174; RAN; 1.
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Matches 208; Conservative
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                                                                             STRAIN=Sprague-Dawley; TISSUE=Brain;
MEDLINE=2210533; PubMed=1319420;
Elferink L.A., Anzai K., Scheller R.H.;
Rabls, a novel low moleular weight GTP-binding protein specifically expressed in rat brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                              WEDLINE=93054572; PubMed=1429617;
Elferink L.A., Anzal K., Scheller R.H.;
Elferink L.A., Anzal K., Scheller R.H.;
-1. Biol. Chem. 267:22693-222693(1992).
-1. FUNCTION: May act in concert with RAB3A in regulating aspects of spraptic vesicle membrane flow within the nerve terminal.
-1. TISSUE SPECIFICITY: Expressed predominantly in neural tissues.
-1. TISSUE SPECIFICITY: Expressed predominantly in neural tissues.
-1. SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro, IPR005220,
( Pfam, PF00071; ras; 1.
R PRINTS, PR0049; RASTRNSFRANG.
)R SMART; SM00175; RAB; 1.
DR TIGRAMS; TIGR00231; small GTP; 1.
CAP-binding; Lipoprotein; Frenylation; Protein transport.

"" RIND 63 67 GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

"A GTP (BY SIMILARITY).

"A GTP (BY SIMILARITY).

"A GTP (BY SIMILARITY).

"A GTP (BY SIMILARITY).

"A GTP (BY SIMILARITY).

"A GTP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 97.5%; Score 1077; DB 1. Best Local Similarity 97.6%; Pred. No. 8.5e-79 Matches 207; Conservative 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; PO5713; 3RAB.
INTERPRO, IPRO03579; GTPase_Rab.
INTERPRO; IPRO01806; Ras trimefrung.
InterPro; IPRO05225; Small_GTP.
                                                                                                                                                                                   Biol. Chem. 267:5768-5775(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 AA; 24283 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M83679; AAA41995.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; F42148; F42148.
                                                            SEQUENCE FROM N.A.
                     NCBI_TaxID=10116;
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207 AA

STANDARD;

RABB_HUMAN ID RABB_HUMAN AC P24407;

RESULT 4

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SECTIS=Human; TISSUE=SKin;

MISDLINE=21388257; PubMed=12477932;

MISDLINE=21388257; PubMed=12477932;

Altachul S.P., Zebebrg B.L., Grouse L.H., Derge J.G.,

Altachul S.P., Zebebrg B., Buetow K.H., Schaefer C.R., Bhat N.K.,

Altachul S.P., Zebebrg B., Buetow K.H., Schaefer C.R., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Mang J., Haith F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Bonaldo M.F., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., McKernan K.J., Malek J.A., Gunzratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu K., Gibbs R.A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEDLINE-91061765; PubMed-2123294;
Chavrier P., Vingron M., Sander C., Simons K., Zerial M.;
"Molecular cloning of YPT1/SEC4-related cDNAs from an epithelial cell

    -!- SUBUNIT: Interacts with MAP4K2 and SYTL4 (By similarity).
    -!- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.

                                                                                                                                                                                                                                                                                          Zahraoui A., Joberty G., Arpin M., Fontaine J.J., Hellio R., Tavitian A., Louvard D.,
Tavitian A., Louvard D.,
"A small rab GTPase is distributed in cytoplasmic vesicles in non
polarized cells but colocalizes with the tight junction marker ZO-1
in polarized epithelial cells.";
J. Cell Biol. 124:101-115(1994).
                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SPECIES-Human; TISSUE-Brain;
Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
"cDNA clones of human proteins involved in signal transduction sequenced by the Gulmine cDNA resource center (www.cdna.org).";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91360267; PubMed=1886711;
Nimmo E.R., Sanders P.G., Padua R.A., Hughes D., Williamson R.,
Johnson K.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The MEL gene: a new member of the RAB/YPT class of RAS-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Cell. Biol. 10:6578-6585(1990).
-!- FUNCTION: May be involved in vesicular trafficking and
neurotransmitter release.
01-WAR-1992 (Rel. 21, Created)
01-WAR-1992 (Rel. 21, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Ras-related protein Rab-8 (Rab-8A) (Oncogene c-mel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                           MEDLINE=94124602; PubMed=8294494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oncogene 6:1347-1351(1991)
                                                                                                            and
                                                                                                                                                                                               CBI_TaxID=9606, 9615;
                                                                                                                                Canis familiaris (Dog)
                                                                                                          Homo sapiens (Human),
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=Human;
                                                                                         WEL OR RABS
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MEDLINE=91115900; PubMed=1899244;
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P51153;
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NP_BIND
NP_BIND
DOMAIN
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ID RB13_HU
DC CCT;
DT 01-0CT;
DT 01-0CT;
DE RAS-rel
GN RAB13.
OC EUKARY
OC MARMANI:
OC MARMANI:
ON IN IN IN IN IN IN SEQUEN
RX MEDLIN
RX MEDLIN
RX ANTELI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 IWDTAGQERFRIITAYYRGAMGIMLVYDITNEKSFDNIRNIRNIRRIERHASADVEKMILG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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Elasmobranchii, Squalea, Hypnosqualea, Pristiorajea, Batoidea,
Torpediniformes, Narcinoidei, Narcinidae, Discopyge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
S-geranylgeranyl cysteine
(By similarity).
LEGNSPQ -> WKATAP (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.3%; Score 545; DB 1; Length 207; 52.9%; Pred. No. 1.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0449; RASTENSFRANG.
SWART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; small GTP; 1.
GTP-binding; Prenylation; Lipoprotein; Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA52DBF54A2CD056 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1991 (Rel. 19, Created)
10-AUG-1991 (Rel. 19, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Ras-related protein Rab-8 (ORA2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001806; Ras trnsfrmng.
InterPro; IPR005225; Small_GTP.
Pfam; PP00071; ras; 1.
                                                                                                                                                                      EMBL; X56741; CAA40065.1; -.
EMBL; S53266; AAB19681.1; -.
EMBL; AF498943; AAM21091.1; -.
EMBL; BC002977; AAM210977.1; -.
EMBL; X56385; CAB56776.1; -.
PIR; B49647; B49647.
HSSP; P05713; 3AAB.
Genew; HGNC;7007; MEL.
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les 99; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
67
124
45
204
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TISSUE=Electric lobe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 RMRASNE 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proto-oncogene.
NP_BIND 15
NP_BIND 63
NP_BIND 121
DOMAIN 37
LIPID 204
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                                                                                                                                                                                                                                                                                                                                                                          MIM; 165040; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
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Matches
    REAL OCCOORDINATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IWDTAGQERFRITTAYYRGAMGIMKVYDITNEKSFDNIKNWIRNIEEHASSDVERMILG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NKADEEÇKROVGREÇGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Ngsee J.K., Elferink L.A., Scheller R.H.; "A family of ras-like GTP-binding proteins expressed in electromotor
                                                                                    J. Biol. Chem. 266:2675-2680(1991).
-!- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
S-gerant/gerantyl cysteine
(By similarity).
(By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.8%; Score 539.5; DB 1; Length 210; 47.4%; Pred. No. 4.5e-36; ative 56; Mismatches 45; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEDILUES-94124602; PubMed=8294494;
Zahraoui A., Joberty G., Arpin M., Fontaine J.J., Hellio R.,
Tavitian A., Louvard D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-00T-1996 (Rel. 34, Created)
01-00T-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ras_related protein Rab-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 RMRASNELALAE-LEEEEGKPEGPANSSK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----NENSLQEAVDKLKSPPKKPSQKKK 201
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, M38391, AA49232.1; -.
PIR, B38625; B38625.
HSSP, POST13; 3RAB.
INCEPPRO; IPRO03579; GTPase Rab.
INCEPPRO; IPRO03579; GTPase Rab.
INCEPPRO; IPRO05225; SMall GTP.
PRINTS; PRO0449; RASTRNSFRNNG.
SMART; SMO0175; Rab; 1.
SMART; SMO0175; Rab; 1.
GGRP-binding; Prenylation; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 AA; 24164 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 4/...
Best Cocal Similarity 5/...
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LIPID
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                                                                                                                                                                                                                            A KENGERLEAGENER,

MEDLINE=22388257; PubMed=12477932;

A trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A trausher R.D., Collins F.S., Wagner L., Shemenc C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

B Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Batchench L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B And S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Asha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Asha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

B Achardes S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

B Ankesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Achigue A.C., Gilmwood J., Schmutz J., Myers R.M.,

B Chnerch A.C., Gilmwood J., Schmutz J., Myers R.M.,

B Cherration and initial analysis of more than 15,000 full-length

B Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

I FUNCTION: Could participate in polarized transport, in the assembly and/or the activity of tight Junctions.

B WITH VESTCLES CATTERED THROUGHOUT THE CYTOPLASM IN CELLS LACKING MITH. THE CYTOPLASM IN CELLS LACKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- TISSUE SPECIFICITY: Detected in several types of epithelia, including intestine, kidney, liver, and in endothelial cells.
-!- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
"A small rab GTPase is distributed in cytoplasmic vesicles in non polarized cells but colocalizes with the tight junction marker ZO-1 in polarized epithelial cells."; cell Biol. 124:101-115(1994).
                                                                                                               Pull H.L. III, Ikeda S.R., Aronstam R.S., elohar clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 602672; -.
60; GO:000523; C:tight junction; TAS.
GO; GO:000328; F:RAB small monomeric GTPase activity; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
GO; GO:0015192; P:vesicle-mediated transport; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTP-binding; Lipoprotein; Frenylation; Protein transport.

NP BIND 12 22 GTP (BY SIMILARITY).

NP BIND 63 67 GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR0013579; GTPABE Rab.
InterPro; IPR001806; Ras trnsfrmng.
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIGRFAMS; TIGR00231; small GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X75593; CAA53266.1; -.
EMBL; AF498948; AAM21096.1; -.
EMBL; BC000799; AAH00799.1; -.
PIR; A49647; A45647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:9762; RAB13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGHT JUNCTIONS.
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                 SEQUENCE FROM N.A.
                                                                                                      TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAKAYDHLFKLLLIGDSGVGKTCLIIRFAEDNFNNTYISTIGIDFKIRTVDIEGKKIKLQ 60
                                                                                                                                                                                                                                                                                              1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUB-Electric lobe;
MEDLINE-9115900; PubMed=1899244;
MEDLINE-9115900; PubMed=1899244;
MSgee J.K., Elferink L.A., Scheller R.H.;
"A family of rae-like GTP-binding proteins expressed in electromotor neurons.";
                                                                                                                                                                                                                                      18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 266:2675-2680(1991).
-!- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Blasmobranchii, Squalea, Hypnosqualea, Pristiorajea, Batoidea,
Torpediniformes, Narcinoidei, Narcinidae, Discopyge.
                     EFFECTOR REGION (BY SIMILARITY).
S-geranylgeranyl cysteine
(By similarity)
141621CB998178DA CRC64;
                                                                                                                                                                       48.1%; Score 532; DB 1; Length 203; 47.6%; Pred. No. 1.7e-35;
                                                                                                                                                                                                                                      43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-geranylgeranyl cysteine
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NP BIND 16 23 GTP (BY SIMILARITY).
NP BIND 122 125 GTP (BY SIMILARITY).
NP_BIND 122 125 GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Discopyge ommata (Electric ray).
                                                                                                                                                                                                                                      49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 RMRASNELALAELEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 GRRSGN-----GNKP--PSTDLKTC 192
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InterPro; IPR003579; GTPase_Rab.
InterPro; IPR01806; Ras trnsfrmng.
InterPro; IPR005225; Small_GTP.
Pfam; PR00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGR00231; small GTP; 1.
                                                                                                                   203 AA; 22774 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M38390; AAA49230.1; -. PIR; A38625; A38625.
                                                                                                                                                                                                                                      Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RB10 DISOM
P22127;
                                                                                                                   SEQUENCE
                                                                                                                                                                              Query Match
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NP_BIND
NP_BIND
                                                                                                                                                                                                          Best Local
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200 AA;
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15-JUL-1999 (Re.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RB10 HUMAN
                   SEQUENCE
                                                            Query Match
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                                                                                                      Matches
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                                                                                                                                                                                                                                                                         60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                  9
                                                                                                                                                                                      1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                                                                               61 QIWDTAGGERFHTITTSYYRGAMGIMLVYDITNAKSFENISKWLRNIDBHANEDVERMLL
                                                                                                                                                                                                                1 MAKKTYDLLFKLLLIGDSGVGKTCVLFRFSDDAFNTFISTIGIDFKIKTVELHGKKIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91061765; PubMed=2123294;
Chavrier P., Vingron M., Sander C., Simons K., Zerial M.;
"Molecular cloning of YPT1/SEC4-related cDNAs from an epithelial cell
                                                                                                                                                 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Céll. Biol. 10:6578-6585(1990).
--- PUNCTTON: May be involved in vesicular trafficking and neurocransmitter relase.
--- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
                                                                                                                                                                                                                                                                                                                                                         120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
S-FECTOR REGION (BY SIMILARITY).
S-Geranylgeranyl cysteine
(By similarity).
S-geranylgeranyl cysteine
                                                                                                        Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTP-binding; Lipoprotein; Frenylation; Protein transport.
NP BIND 16 23 GTP (BY SIMILARITY).
NP BIND 64 68 GTP (BY SIMILARITY).
NP_BIND 122 125 GTP (BY SIMILARITY).
                                                                                                                                                 30; Indels
             (by biminatity).
Segeranylegranyl cysteine.
(By similarity).
41D38E3D760519C5 CRC64;
                                                                                                      48.1%; Score 531.5; DB 1; 56.4%; Pred. No. 1.8e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
00-CT-2003 (Rel. 42, Last annotation update)
Ras-related protein Rab-10.
  (By similarity)
                                                                                                                                                 44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X56387; CAA39798.1; -.
PIR; D36364; D36364.
HSSP; P05713; 3RAB.
InterPro; IPR003579; GTPase Rab.
InterPro; IPR001806; Ras trnsfrmug.
InterPro; IPR005225; Small_GTP.
Pfam; PP00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
TIGRFAMB; TIGR00231; small_GTP; 1.
                                                                 200 AA; 22623 MW;
                                                                                                                                                 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23
68
125
46
199
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                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
122
38
199
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                          199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CANFA
                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CANFA
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                          LIPID
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60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
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SPECIES=Human, TISSUS=Pituitary;

HU R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,

Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,

Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J.,

Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,

Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;

"Gene expression profiling in the human hypothalamus-pituitary-adrenal
axis and full-length cDNA cloning.";

Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatesuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                         1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 GNKADEEOKROVGREOGOGLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-Human, TISSUB-Brain,
Publ H.L. III, Ikeda S.R., Aronstam R.S.;
Fignal clones of human proteins involved in signal transduction
sequenced by the Guthrie cDNA resource center (www.cdna.org).";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                            1,
                                                                                        48.0%; Score 530.5; DB 1; Length 200; 55.8%; Pred. No. 2.2e-35; ive 46; Mismatches 29; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wong K., Hong W., Tang B.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
(By similarity).
5D52B8E8E47D4362 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ras related protein Rab-10.
                                 22569 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SPECIES=Human; TISSUE=Cervix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human), and
                                                                                                                                                                   96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606, 10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Mouse)
                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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transport

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MEDINE-2238257; PubMed=12477932;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Schemen C.M., Schuler G.D.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Schemen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Stapleton M., Soares M.B., Donaldo M.F., Carino B.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

A Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

W Villalon D.K., Munny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

W Wilting M.M., Raden A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Schemutz J., Myers R.M.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 QIWDTAGQERFHTITTSYYRGAMGIMLVYDITNGKSFENISKWLRNIDEHANEDVERMLL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAKKTYDLLFKLLLIGDSGVGKTCVLFRFSDDAFNTTFISTIGIDFKIKTVDLQGKKIKL
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                              GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
S-geranylgeranyl cysteine
(By similarity).
S-geranylgeranyl cysteine
(By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.0%; Score 530.5; DB 1; Length 200; 55.8%; Pred. No. 2.2e-35; Live 46; Mismatches 29; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Fetal brain;
Seki N., Saito T.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                     PY SIMILATICY).

-> H (IN REF. 7).

7F02B8E8E46EE1E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RB8B_HUMAN STANDARD; PRT; 207 AA. 092931, 15-UZL-1999 (Rel. 38, Created) 15-UZC-2001 (Rel. 40, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) RBS_Telated protein Rab-8B.
                                                                                                                                                                                                                                                                                                                                                                                                                                      N -> H (IN REF.
InterPro; IPR001806; Ras trnsfrmng.
InterPro; IPR00525; Small_GTP.
Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRNNG.
SMART; SM00175; RAB; 1.
TIGREAMS; TIGR00231; small_GTP; 1.
GTP-binding; Lipoprotein; Prenylation; Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                              22541 MW;
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Matches 96; Conservative
                                                                                                                                                                                                          23
68
125
199
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NP_BIND
NP_BIND
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES—Mouse, STRAIN=C57BL/6J; TISSUE=Stomach;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kando S., Yamanaka I.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

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Radota K., Matsuda H.A., Gissi C., King B., Kochiwa H.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fuljita M., Gariboldi M.,

Ausonstein M.J., Bult C., Pletcher C., Fuljita M., Gariboldi M.,

Ausonstein M.J., Bult C., Restoher C., Fulli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Radriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wunshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                 Attaubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Haich R.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Caraninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A. Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmucz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               varure 409:689-690(2001).
-!- FUNCTION: May be involved in vesicular trafficking and
neurotransmitter release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=Mouse; Zeng Q., Tan Y.H., Hong W.; Zeng Q., Tan Y.H., Hong W.; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
     MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003579; GTPase Rab
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AF035646; AAC29313.1;
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HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AK023223; BAB14474.1;
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MGD; MGI:105066; Rab10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001)
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EMBL; AF035646;
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53 9

Gaps

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
Ras-related protein Rab-8 (Oncogene c-mel).
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                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003579; GTPase Rab.
InterPro; IPR001806; Ras trnsfrmng.
InterPro; IPR005225; Small_GTP.
                                                              SEQUENCE FROM N.A.
MEDLINE=96393028; PubMed=8799816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 AA; 23603 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00071; ras; 1
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Best Local Similarity
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                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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01-OCT-1996 (
01-OCT-1996 (
10-OCT-2003 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NP BIND
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                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 IWDTAGGERFRITTAYYRGAMGIMLVYDITNEKSFDNIKNWIRNIEBHASSDVERMILG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 NKADEEOKROVGREQGQQLAKEYGMDFYETSACTNLNIKES-PTRLTELVLQAHRK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen D., Guo J., Gahl W.A.;
"RAB GTPases expressed in human melanoma cells.";
Biochim. Biophys. Acta 1355:1-6(1997).
-!- FUNCTION: May be involved in vesicular trafficking and
neurotransmitter release (By similarity).
-!- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGKFAMS; IIGKUUGJI; BURGIL JUFF; 1.

GTP-binding; Premylation; Lipoprotein; Protein transport.

NP BIND 12 22 GTP (BY SIMILARITY).

NP BIND 121 124 GTP (BY SIMILARITY).

NP BIND 121 124 GTP (BY SIMILARITY).

NP BIND 204 204 S-GEFECTOR REGION (BY SIMILARITY).

LIPID 204 204 S-GETANJIGHTIN, CYBLEINE (BY SIMILARITY).

SEQUENCE 207 AA; 23584 MW; 5960993COF87F944 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.8%; Score 528.5; DB 1; Length 207; 54.0%; Pred. No. 3.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0003928; F:RAB small monomeric GTPase activity; NAS. GO; GO:0015031; P:Protein transport; NAS. InterPro; IPR003579; GTPase Rab. InterPro; IPR001806; Ras trinsfrung. InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Indels
                                       numan and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ras-related protein Rab-8B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
TIGRFAMB; TIGR00231; small_GTP; 1.
                                                                                                                                       AEDLINE=97182150; PubMed=9030196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB038995; BAA92249.1; -. EMBL; BC020654; AAH20654.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U66624; AAC51199.1; -. HSSP; P05713; 3RAB.
                                                                                                  SEQUENCE OF 67-119 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                       rissue=Melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RB8B RAT
P70550;
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RESULT 11 RB8B RAT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKES-FTRLTELVLQAHRK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                                                                                             -i- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.8%; Score 528.5; DB 1; Length 207; 54.0%; Pred. No. 3.3e-35; ive 47; Mismatches 33; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

EFFECTOR REGION (BY SIMILARITY).

S-geranylgeranyl cysteine

(By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
TIGREAMS; TIGR00231; Small GPP; 1.
GTP-binding; Prenylation; Lipoprotein; Protein transport.
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SCHPO
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           YPT2 SCHPO
ID YPT2 SCH
AC P17609;
 RESULT 13
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                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
                                                                                                                       STRAIN-BALB/c; TISSUE-Melanoma;
MEDLINE-96209873; PubMed-8643544;
Ren M., Zeng J., De Lemos-Chiarandini C., Rosenfeld M., Adesnik M.,
                                                                                                                                                                              In its active form, the GTP-binding protein rab8 interacts with a
MEDLINE=91360267; PubMed=1886711;
Nimmo E.R., Sanders P.G., Padua R.A., Hughes D., Williamson R.,
Johnson K.J.;
                                             The MEL gene: a new member of the RAB/YPT class of RAS-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
S-geranylgeranyl cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.6%; Score 526; DB 1; Length 206; 56.4%; Pred. No. 5.2e-35; live 41; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMS; TIGR00231; small GTP; 1.
GTP-binding; Prenylation; Lipoprotein; Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (By similarity).
49D832725D662942 CRC64;
                                                                                                                                                                                                 stress-activated protein kinase.";
Proc. Natl. Acad. Sci. U.S.A. 93:5151-5155(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:96560; Mel.
GO; GO:0005515; F:protein binding; IPI.
InterPro; IPR001879; GTPase Rab.
InterPro; IPR001806; Ras trinsfrung.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                           INTERACTION WITH SYTL4.
MEDLINE=22590467; PubMed=12590134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00449; RASTRNSFRMNG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; S53270; AAB19682.1; -. HSSP; P05713; 3RAB.
                                                                         Oncogene 6:1347-1351(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 56.**.
Best Local Similarity 56.**.
Conservative
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                                                                                                       INTERACTION WITH MAP4K2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22
67
124
45
203
                                                                                                                                                                     Sabatini D.D.;
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                                                             qenes.";
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NP_BIND
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Mood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,

Mood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,

Squros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

A Collins M., Comnor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

A Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,

A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

A Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA James K., Jones M., Leather S., McDonald S.,

Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Rutherford K., Rutter S., Saunders D., Scherens K.,

Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitchead S.,

Roberton J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Rodyard J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Rodyard J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Robitjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

Rablibert F., Aves S.J., Kiang Z., Hunt C., Moore K., Hurst S.,

Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

Ralibert F., Aves S.J., Kiang Z., Hunt C., Moore K., Hurst S.,

A Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

Ramiguez A., Revuelta J.L., Moreno S., Ammstrong J., Forsburg S.L.,

Ramiguez A., Revuelta J.L., Moreno S., Ammstrong J., Forsburg S.L.,

Ramiguez A., Revuelta J.L., Moreno S., Ammstrong J., Rotashkin J.,

Rhyakovski G.V., Ussery D., Barrell B.G., Nurse P.;

The genome sequence of Schizosaccharomyces pombe.";

Rutre 415:871-880(2002).

LI-FUNCTION: Protein transport. Probably involved in vesicular

Reger P., Stander M., Sandaria I. For ell vishility.

Reger P., Matter P., Wester P., Matter P., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     essential ras-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- MISCELLANEGUS: This protein is essential for cell viability.
-!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAB FAMILY.
PROBABLE YEAST SEC4 HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                    Hengst L., Lehmeier T., Gallwitz D.;
"Structural and functional analysis of ypt2, an essential ras-relate
gene in the fission yeast Schizosaccharomyces pombe encoding a Sec4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pawell B., Hook S., Sweet D., Armstrong J.;
"Novel YPT1-related genes from Schizosaccharomyces pombe.";
Nucleic Acids Res. 18:4264-4264 (1990).
                                                                                                                                                                                                        Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae;
                                              01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
200 AA.
                                                                                                                                                    YPT2 OR SPAC9E9.07C. Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90332438; PubMed=2115995;
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90269232; PubMed=2112089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBO J. 9:1957-1962(1990).
                                                                                                                              Ras-related protein ypt2.
                                                                                                                                                                                                                                                               Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein homologue.
                                                                                                                                                                                                                                                                                           NCBI TaxID=4896;
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oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILJGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 - EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRMR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
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P28186;
01-DEC-1992 (Rel. 24, Created)
10-DCT-2003 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 24, Last annotation update)
10-OCT-2003 (Rel. 24, Last annotation update)
ARAJAGOPSIS (Rel. 24, Last annotation update)
ARAJGOPSIS (Nouse-ear cress).
BUKATYOTA; VITIGIPIANTAS; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Guicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation and analysis of cDNAs encoding small GTP-binding proteins of Arabidopsis thaliana.";
Gene 108:259-264(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=cv. Landsberg erecta, cv. Columbia, cv. En-1, cv. Lapalmam,
and cv. Estland;
TISSUE=Loaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92084144; PubMed=1748311;
Anai T., Hasegawa K., Watanabe Y., Uchimiya H., Ishizaki R.,
Matsui M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 46.1%; Score 509; DB 1; Length 215; Best Local Similarity 47.8%; Pred. No. 1.2e-33; Matches 100; Conservative 42; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                        GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

S-geranylgeranyl cysteine
(By similarity).

S-geranylgeranyl cysteine
(By similarity).
  and this statement is not removed.
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                                                                                                                                                                                                                                                                          PRINTS; PRO0449; RASTRNSFRWNG.
SWART; SM00175; RAB; 1.
TIGRRAMB; TIGRO0231; small_GTP; 1.
GTP-binding; Lipoprotein; Frenylation.
NP_BIND 22 29 GTP (BY SIM)
NP_BIND 70 74 GTP (BY SIM)
LIPID 212 212 S-geranylges
                                entities requires a license agreement (
or send an email to license@isb-sib.ch)
                                                                                                                                                                          InterPro; IPR003579; GTPase Rab.
InterPro; IPR001806; Ras trinsfrung.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 AA; 23787 MW;
                                                                                                  EMBL; Z49152; CAA89021.1; -.
PIR; T14565; T14565.
HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213
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STRAIN=cv. Columbia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 CDCEDQRQVSFEQGQALADELGVKFLEASAKTNVNVDEAFFTLA------REIKKQKI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTAGOERYQTITKOYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 ADEEQKRQVGREQGQQLAKEYGMDFYETSACTNINIKESFTRLTELVLQAHRKELEGLRM 182
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SEQUENCE FROM N.A.
STRAIN=CV. D100 KS 38080;
STRAIN=CV. D100 KS 38080;
MEDLINE=96507523; PubMed=8680960;
MEDLINE=96507523; PubMed=8680960;
Dallery E., Quief S., Ben Jilany K.E., Kerckaert J.-P., Hagege D.;
"Molecular cloning and structural analysis of cDNAs that encode 3
small GTP-binding proteins from sugar beet.";
C. R. Acad. Sci., III, Sci. Vie 319:91-97(1996).
C. R. Acad. Sci., III, Sci. Vie 319:91-97(1996).
-!- SIMILARITY: Belongs to the small GTPase superfamily.
--- T is produced through a collabor
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
NCBI_TaxID=161934;
          GeneDB SPOWDe; SPACESB.07c; -.

GeneDB SPOWDe; GFPACEB.07c; -.

DR InterPro; IPR0013679; GTPACEB.D.

DR InterPro; IPR0013679; GTPACEB.D.

DR PEam; PF00071; ras; 1.

DR PRINTS; PR00449; RASTRNSFRWNG.

DR SWART; SW00175; RAB; 1.1

DR TIGREAM; TIGROLO31; small GTP; 1.

FT NP BIND 16 23 GTP (BY SIMILARITY).

FT NP BIND 64 68 GTP (BY SIMILARITY).

FT DOWAIN 38 46

T LIPID 100
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                                                                                                                                                                                                                                                                                                                                                          GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
BPFECTOR REGION (PROBABLE).
S-geranylgeranyl cysteine.
(By similarity).
S-geranylgeranyl cysteine.
(By similarity).
W; 2C658D153A290C30 CRC64;
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15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 AA; 22755 MW;
  EMBL; X52864; CAA37045.1; -. EMBL; X52864; CAA37045.1; -. EMBL; S99262; CAB16405.1; -. PIR: S17701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ras-related protein RABIBV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta vulgaris (Sugar beet)
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RAB1_BETVU
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Ratimann B., Valle G., Bloecker H., Perez-Alonso M., Obernaier B.,
Ratimann B., Valle G., Bloecker H., Perez-Alonso M., Obernaier B.,
Ra Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
Ra Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
Ra Mincker P., Cattolico L., Weissenbach J., Saurin W., Obetier P.,
Ra Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Banger V.,
Ra Wurmbach E., Drzonek H., Voss H., Holland R., Brandt P., Nyakatura G.,
Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
Norado A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
Raichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
Ravarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
Ravarro P., Collado C., Perez-Perez A., Ottenwaelder B., Masuy D.,
Rocke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
Androfort A., Argirtou A., Plores M., Liguorin R., Vitale D.,
Annhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
Raper K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
Rochey T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
Presser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu B.,
Riyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Riyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Ryokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Ryokawa C., Kamada M., Yasuda M., Tabata S.,
Haliana W.,

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    -!- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.

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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
STECTOR REGION (BY SIMILARITY).
S-geranylgeranyl cysteine
(By similarity).
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S-geranylgeranyl cysteine (By similarity).
(09E9C19A7A44E705 CRC64;
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InterPro; IPR001806; Ras trinsfrung.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; xas; 1.
MEDLINE=21016720; PubMed=11130713;
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SMART; SM00175; RAB; 1.
FIGRFAMS; TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D01025; BAA00830.1; -.
EMBL; AL355775; CAB90933.1; -.
PIR; JS0640; JS0640.
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Best Local Similarity 46.9%
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 408:820-822(2000).
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125 - BEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRMR 183
                                                                      184 ASNELALAE-----LEBEBGKPEGPANSSKTC 210
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Q91yw0 mus musculu Q81yw89 homo sapien Q71344 brachydanio Q91y82 caenorhabdi O15971 drosophila Q8Vcf6 mus musculu Q8A3x5 rattus norv O18338 drosophila Q9h0t3 homo sapien Q9d003 mus musculu Q9het4 asperqillus Q2het4 asperqillus Q7xhp7 oryza sativ Q40215 lotus japon Q940215 lotus japon Q9fjf1 arabidopsis
                                                March 15, 2004, 11:12:33 ; Search time 46 Seconds (without alignments) 1454.127 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                    1 MAKQYDVLFRLLLIGDSGVG.....LEEEEGKPEGPANSSKTCWC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                 1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                  OM protein - protein search, using sw model
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Q8VCF6
Q8K3X5
O18338
Q9H0T3
Q9DD03
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Q8IW89
Q7T3A4
Q9TYS2
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Q40218
Q7XHP7
Q40215
Q9FJF1
                                                                                                                                                                                                                                                                                                                                           sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_nvertebrate:*
sp_mammal:*
sp_mnc:*
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sp_phage:*
sp_plant:*
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sp_bacteriap:*
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Maximum DB seq length: 200000000
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Match Length DB
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46.9
46.9
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Perfect score:
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ALIGNMENTS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

Last sequence update)
Last annotation update)

01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-OCT-2003 (TrEMBLrel. 25, Hypothetical protein.

Mus musculus (Mouse)

SEQUENCE FROM N.A. NCBI TaxID=10090;

Created) PRT;

168

PRELIMINARY;

PRINTS; PRO0449; RASTRNSFRANG.
SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR0021; small GTP; 1.
PROSITE; PS00675; SIGM54 INTERACT 1; 1.
HYDOCHELICAL protein; GPP-binding; Lipoprotein.
SEQUENCE 168 AA; 19399 MW; 4E2C2FBIC56ECDF8 CRC64;

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121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNINIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Mismatches
                                                         R-MRASNELALAELEEEEG 198
                                                                                169 RLMRSRN----GRWEESKG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 102; Conservative
                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Kidney;
                                                                                                                                                                                                                                                                                           TISSUE=Kidney
                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
                                                                                                                                         Q7T3A4
                                                                                                                  RESULT 3
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                                                                                                          61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                           61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDE------VG 113
                                                                                                                                                                                                                                                                                                                                                                       1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIDVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                               1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Gaps
                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                         ö
Query Match 72.2%; Score 798; DB 11; Length 168; Best Local Similarity 99.3%; Pred. No. 5.2e-60; Matches 152; Conservative 1; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.9%; Score 573; DB 4; Length 211; 62.8%; Pred. No. 9e-41; tive 15; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 AA; 23761 MW; 3BFA7CF89D4DF54F CRC64;
                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                         121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSAC 153
                                                                                                                                                               121 NKADEEOKROVGREOGOOLAKEYGMDFYETSAC 153
                                                                                                                                                                                                                         211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMB; TIGR00231; small_GTP; 1.
PROSITE; PS00675; SIGMA54_INTERACT_1; 1.
                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002041; RAN.
InterPro; IPR001086; Ras trnsfrmng.
InterPro; IPR002078; 31954 interact.
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                             Hypothetical protein (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003579; GTPase Rab.
InterPro; IPR003577; GTPase Ras.
InterPro; IPR003578; GTPase Rho.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0449; RASTRNSFRMNG.
SWART; SM00175; RAB; 1.
SWART; SM00173; RAS; 1.
SWART; SM00173; RAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 62.8%,
Matches 125; Conservative
                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
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                                                                                                                                                                                                                                     QBIWB9;
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61 INDIAGOERYQTITKOYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLT-ELVLQAHRK 175
                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.0%; Score 563.5; DB 13; Length 200; 58.0%; Pred. No. 5.4e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC053195; AAH53195.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 200 AA; 22458 MW; FA177CEDAEF2820C CRC64;
                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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015971
015971;
                                                               RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NKCDIEERREVSRDRGEQLAIEYGTKFLETSAKANLNIDEAFFTLARDI----KSKMEON 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WormPep; D1037.4; CE30273.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0005525; F:GTP binding; IEA.

GO; GO:0003928; F:RAB small monomeric GTPase activity; IEA.

GO; GO:00015031; P:PROTE mil missport; IEA.

GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.

GO; GO:000160; P:two-component signal transduction; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Gaps
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
EMBL; AF106592; AAX21367.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

50.4%; Score 557; DB 5; Length 211;
Best Local Similarity 55.0%; Pred. No. 2.1e-39;
Matches 104; Conservative 42; Mismatches 39; Indels
                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
C. elegans RAB-8 protein (corresponding sequence D1037.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ledwith J., Biewald T., "The sequence of C. elegans cosmid D1037."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00675; SIGMAS4_INTERACT_1; 1.
GTP-binding; Lipoprotein.
SEQUENCE 211 AA; 24022 MW; B7609A91B6082DA2 CRC64;
                                                               211 AA.
                                                                                                                                                                                                                                                                                                                              Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002078; Sig54_interact.
InterPro; IPR005255; Small_GTP.
Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001806; Ras trnsfrmng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003579; GTPase Rab
                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
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TIGRFAMS; TIGR00231; sm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston R.:
                                                               Q9TYS2
RESULT 4
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RA Adams M.D., Celniker S.E., 1401 R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., 1401 R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., 1401 R.A., Fvans C.A., Galle R.F.,
Gocaye R.A., Lewis S.E., Richards S., Amburner M., Henderson S.N.,
RA Sutron G.G., Wortnan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutron G.G., Wortnan J.R., Earler E.G., Champe M., Pfeiffer B.D.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barla J.E., Agbayain A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beeson K.Y., Basu A., Baxendala J., Baytaktarollu L., Beasley B.M.,
RA Beeson K.Y., Banch R.P., Bulandari D., Bolahakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodgon K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dodgon K.J., Evangelista C.C., Ferraz C., Ferriera S., Pleicz Chman M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchun K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchun K.A.,
Liuk C., Mattei B., McIntoen T.C., McIeod M.P., McPherson D.,
Reitchio W., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Ralazolo M., Pittenan G.S., Pan S., Pollard J., Mouth S.M.,
Rules D., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
Rander S., Woodage T., Worley K.C., Wu D., Yang S., Zho O.A.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zho O., Andriba R.A., Whyers B.W., Rubin G.M., Venter E., Willen W., Saith H. W.,
R. The genome sequence of Drosophila melanogaster.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Satch A.K., Tokunaga F., Ozaki K.; "Rab proteins of the Rab-"Rab proteins of Drosophila melanogaster: novel members of the Rab-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                              Last sequence update)
Last annotation update)
                                       01-JAN-1998 (TrEMBLrel. 05, Created)
                                                                                                                                                                                                                                                                                                              STRAIN=Berkeley;
MEDLINE=20196006; Pubmed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-OREGON R; TISSUE=Head;
MEDLINE=97228579; PubMed=9074639;
                                                       01-JAN-1998 (TrEMBLrel. 05, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                        RAB10 protein (LD39986P).
RAB10 OR DRAB10 OR CG17060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EBS Lett. 404:65-69(1997).
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PRELIMINARY;
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61 IWDTAGQERYQTITKQYYRRAQGIFLUYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     testis.;
Submitted (JUN-2012) to the EMBL/GenBank/DDBJ databases.
EMBL; AF525280; AAM82581;
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003525; F:GTP binding; IEA.
GO; GO:0003938; F:RAB small monomeric GTPase activity; IEA.
GO; GO:0003931; F:RAS small monomeric GTPase activity; IEA.
GO; GO:0003931; F:RAS small monomeric GTPase activity; IEA.
GO; GO:0003931; F:RAS small monomeric GTPase activity; IEA.
GO; GO:0000386; P:intracellular protein transport; IEA.
GO; GO:000166; P:small GTPase mediated signal transduction; IEA.
GO; GO:000166; P:wo-component signal transduction system (p. .; IEA.
InterPro; IPR006688; ARP.
   transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAXTYDYLFKLLLIGDSGVGKTCVLFRFSEDAFNSTFISTIGIDFKIRTIELDGKRIKLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Lau A.S.N., Cheng C.Y., Mruk D.D.;
"Rabl3 participates in Sertoli cell tight junction assembly in
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                       BELONGS TO THE RAB SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                49.0%; Score 541; DB 11; Length 207; 50.3%; Pred. No. 4.6e-38; ive 49; Mismatches 49; Indels (
                                                                                                                                                                                                                                                                                                                                                                            207 AA; 23668 MW; AC89DC85588FB8F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 AA.
                                                                                                                                                                                                                                                                                                        SMART, SM00175; RAB; 1.
TIGRFAMS; TIGR00231; small GTP; 1.
PROSITE; PS00675; SIGMAS4 INTERACT 1; 1.
                                                                                                                                                                        GO; GO:0005515; F:protein binding; IPI.
InterPro; IPR003579; GTPasse_Rab.
InterPro; IPR001806; Ras trnsfrmng.
InterPro; IPR002078; Sig54 interact.
InterPro; IPR005225; Small_GTP.
PERM; PP00071; Tas; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                   -i- SIMILARITY: TO RAS PROTEINS.
EMBL; BC019990; AAH19990.1; -.
EMBL; AK076048; BAC36146.1; -.
EMBL; AK079306; BAC37603.1; -.
EMBL; AK080740; BAC38003.1; -.
HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 RMRASNELALAELEEEE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 SPQGSSHGVKITVEQQK 197
                                                                                                                                                                                                                                                                                       PRINTS; PR00449; RASTRNSFRMNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2003 (TrEMBLrel. 25, GTP-binding protein RAB13.
   "Analysis of the mouse trans
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 50.3%;
Matches 99; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                 GTP-binding; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat)
                                                                                                                                                                 MGD; MGI:96960; Mel. GO; GO:0005515; F:pr
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                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 QIWDTAGQERPHIITISYYRGAMGIMLVYDITNEKSFENIVKWLRNIDEHANEDVEKMIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 GNKADEBOKROVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59
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                                                                                                                        FlyBase, FBGT0015789; Rablo.

GO; GO:0005527; F:DNA binding; IEA.

GO; GO:0005225; F:GTP binding; IEA.

GO; GO:0001928; F:RAB small monomeric GTPase activity; IEA.

GO; GO:0001564; F:RAB small monomeric GTPase activity; IEA.

GO; GO:0001569; F:RAB small GTPase mediated signal transduction; IEA.

GO; GO:000160; P:two-component signal transduction system (p. . .; IEA.

InterPro; IPR001579; GTPase Rab.

InterPro; IPR001606; Ras_trnsfrmng.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN Genome Exploration Research Group Phase I & II Team;
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
5imilar to mel transforming oncogene (Derived from cell line NK14)-RAB8 homolog (Cell line NK14 derived transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                           TIGREAMS; TIGR00231; small GTP; 1.
PROSITE; PS00675; SIGMAS4 INTERACT 1; 1.
GTP-binding; Lipoprotein.
SEQUENCE 204 AA; 23336 MW; 4E058761C6854920 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUB=Body, Cerebellum, and Retina; MEDLINE=22354683; PubMed=12466851; The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.5%; Score 546.5; DB 549.8%; Pred. No. 1.5e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47; Mismatches
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                                                                                                                                                                                                                                                                     InterPro; IPR001806; Ras trnsfrmng.
InterPro; IPR002078; Sig54 interact.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
                                                   PRINTS; PR00449; RASTRNSFRMNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 49.8%;
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                               SMART; SM00175; RAB; 1
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'EBS Lett. 404:65-69(1997).
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A Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Galle R.F.,
A Gocage R.A., Lewis S.E., Fichards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Man K.H., Doyle C., Baxer B.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baddin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bulck J., Cadieu E., Center A., Chandra I.,
A Burtis K.C., Busam D.A., Bulter H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Dodson K., Doup L.B., Downes M., Duga R.D., Dew I., Dietz S.M.,
A Durbin K.J., Evangelista C.C., Ferriar S., Fleischmann W.,
                                                                                                                                                                                                                                                                                                                                                        61 IMDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                      1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                9; Gaps
                                                                                                                                                                                                                                       DB 11; Length 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                               46; Indels
                                                                                                                                                                                                              203 AA; 22901 MW; B6687462C6EA95A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RABS protein (LD44762p).
                                                                                                                                                                                                                                    Query Match
47.8%; Score 528.5; DB 1:
Best Local Similarity 48.1%; Pred. No. 5.2e-37;
Matches 100; Conservative 53; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                             RMRASNELALAELEEEGKPEGPANSSK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 RSGNSSKPSSTDLKVSDKK----NSNK 199
                                                                                                                                                                       TIGRFAMS; TIGR00231; small GTP; 1.
PROSITE; PS00675; SIGMAS4 INTERACT 1; 1.
GTP-binding.
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                                               InterPro; IPR001806; Ras trnsfrmng.
InterPro; IPR002078; Sig54 interact.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20196006; PubMed=10731132;
                       GTPase_Rho.
             GTPase Ras
GTPase Rab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                         SMART; SM00177; ARF; 1.
SMART; SM00175; RAB; 1.
SMART; SM00176; RAB; 1.
SMART; SM00173; RAS; 1.
SMART; SM00174; RHO; 1.
                       InterPro; IPR003578;
                                    InterPro; IPR002041;
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                                                                                                                                                                                                                 SEQUENCE
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Repeter C., Gentralian A.R., Garrell J.H., Gui Z., Genhart W. Glasser K., Glodel K. Glodel K. Grong F., Gorrell J.H., Gui Z., Genhar P., Harris W. H., Gui Z., Genhar P., Harris W. H., Harris W. L., Harry D., Harris W. H., Harry D., Ha
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                      0610007N03RIK.
                                                                                     Q9DD03;
Q9DD03;
01-JUN-2001
                                           RESULT 10
Q9DD03
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61 IMDTAGQERFRIITAYYRGAMGIMLVYDITQEKSFENIKNWIRNIEENASADVEKMLLG 120
                                                                                            60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003282; F:GTP binding; IEA.
GO; GO:0003282; F:RAB small monomexic GTPase activity; IEA.
GO; GO:0015031; P:protein transport; IEA.
GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
GO; GO:000160; P:two-component signal transduction system (p. .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAKKTYDLLFKLLLIGDSGVGKTCVLFRFSDDAFNTTFISTIGIDFKIKTVELQGKKIKL
                                                                NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.; Tymards a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: TO RAS PROFEINS, BELONGS TO THE RAB SUBFAMILY L; AL136650; CAB66585.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGRO0231; small GTP; 1.
PROSITE; PS00675; SIGMAS4 INTERACT 1; 1.
Hypothetical protein; GTP-blinding Lipoprotein.
SEQUENCE 200 AA; 22469 WW; 7F01DB88B46EE3EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.6%; Score 526.5; DB 4
55.8%; Pred. No. 7.5e-37;
tive 45; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                          Created)
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InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
MEDLINE=21154917; PubMed=11230166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interPro; IPR003579; GTPase Rab.
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01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein.
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Les 96, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                        181 RMRASN 186
                                                                                                                                                                                                    176 RMEANN 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                       Q9H0T3;
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Matches
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Rawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A hizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Brownstein M.J., Bult C., Fletcher C., Pujita M., Gariboldi M.,
Chustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Iyons P., Marchionni L., Machima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Rinnayald M., Rodriguez I., Sakamoto N.,
Nordone P., Ring B., Rinnayald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAKAYDHLFKILLIGDSGVGKTCLIIRFAEDNFNSTYISTIGIDFKIRTVDIEGKRIKLQ 60
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                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0003928; F:RAB small monomeric GTPase activity; IEA.
GO; GO:0015031; P:protein transport; IEA.
GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
GO; GO:0000160; P:two-Component signal transduction system (p. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
--- SINTLARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
EMBL; AK002303; BAB222000.1; ---
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PROSITE; PS00675; SIGMAS4_INTERACT_1; 1.
GTP-binding; Lipoprotein.
SEQUENCE 202 AA; 22770 WW; SDF599432E228AC0 CRC64;
                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 0610007N03Rik protein (RIKEN cDNA 0610007N03 gene).
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54.1%; Pred. No. 8.4e-37;
iive 45; Mismatches 33;
                                                                             Created)
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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0005525; F:GTP binding; IEA.
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InterPro; IPR002078; Sig54 interact
InterPro; IPR005225; Small GTP.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P05713; 3RAB.
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Best Local Similarity
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Quetier F.,

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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003525; F:GTP binding; IEA.
GO; GO:000325; F:Small monomeric GTPase activity; IEA.
GO; GO:000326; F:Small GTPase mediated signal transduction; IEA.
GO; GO:000160; P:two-component signal transduction system (p. . .; IEA.
InterPro; IPR001806; Ras trnsfrmug.
InterPro; IPR002078; Sig54_interact.
InterPro; IPR005225; Small_GTP.
           GTPase ALEARB (At3g53610).

RABB OR F4P12 310.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P., Chan M., Chang C.H., Dale J.M., Hayashizaki Y., Hauan V.W., Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hauan V.W., Ishida J., Jones T., Kaniya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Sarou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hags B.G., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                   Bloecker H., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.,
Salanoubat M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell
Feldmann K.;
"Full-Length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Subhitted (FEB-2003)

BMBL, 108244; AAB65088.1; -.

EMBL, AL132966; CAB6768.1; -.

EMBL; AY086756; AAM63807.1; -.

EMBL; AY086779; AAM648045.1; -.

EMBL; H5901; T45901.

HSSP; P05713; 3RAB.
                                                                                                                                                               SEQUENCE FROM N.A.
STRALT-GO. Columbia;
Bischoff F., Palme K.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 AA; 23939 MW; 1648E45B29D4EEB6 CRC64;
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.0%; Score 519; DB 10; ilarity 51.9%; Pred. No. 3.6e-36; Conservative 42; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMS; TIGR00231; small_GTP; 1.
PROSITE; PS00675; SIGMAS4_INTERACT_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00449; RASTRNSFRMNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Biol. 0:0-0(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       annotation.
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6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Punt P.J., Seiboth B., Weenink X.O., van Zeijl C.M., Lenders M., Konetschny C., Ram A.F., Montijn R., Kubicek C.P., Van Den Hondel C.A., Eam A.F., Montijn R., Kubicek C.P., Van Den Hondel C.A., Montijn R., Kubicek C.P., Van Den Hondel C.A., Eastering and characterisation of a family of secretion related small GTPase encoding genes from the filamentous fungus Aspergillus niger: a putative SEC4 homologue is not essential for growth."; L. Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
1. SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY. RMBL, ALJ78658; CAC17832.1; R. HSSP; P05713; JRAB.
R GO; GO:0005255; F:GTP binding; IEA.
RO; GO:00103289; F:RAB small monomeric GTPase activity; IEA.
R GO; GO:0010264; P:RMBl CTPBER Mediated signal transduction; IEA.
                                    61 VWDTAGQERFKTITTAYYRGAMGIILVYDITDEKSFENIQNWMKSIKENASAGVERLLLG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 DTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTAGGERFRIITTAYYRGAMGILLVYDVTDERSFQNIRTWFSNVEQHASEGVHKILIGNK 124
                 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 KQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                            Aspergillus niger.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                        121 NKADEBOKROVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVL 170
                                                                                                           47.1%; Score 521; DB 3; Length 206; 60.6%; Pred. No. 2.3e-36; tive 30; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTP-binding; Lipoprotein.
SEQUENCE 206 AA; 22823 MW; 501916B795CF8CBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 ADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESF 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDWEEKRAVSTEQGQQLANELGIPFLEVSAKNNINIEKAF 164
                                                                                                                                                                                                                                                     01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR0013579; GTPBSBE Rab.
InterPro; IPR001806; Ras trisfrang.
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00175; RAB; 1.
TIGRFAMB; TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                 Secretion related GTPase, (SrgA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
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                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=N402;
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Matches
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024466
ID 02446
AC 02446
DT 01-JA
DT 01-JA
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YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKWKTIEVDGIWDT 43; Indels

Length 216;

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132 MDESKRAVPTSKGQALADEYGIKFFETSAKTNLNVEEVFFSIARDIKQRLADTDHKAEPT 191
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46.9%; Score 518; DB 10;
Best Local Similarity 47.5%; Pred. No. 4.4e-36;
Matches 103; Conservative 42; Mismatches 48;
                                                                                      --- AANKSSCC 213
                                                                                                                                                                                                      215 AA.
                                          179 GLRMRASNELALAELEEEGKPEGPANSSKTC
                                                                                                                                                                                                                                                  Created)
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01,
25,
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                                                                                      192 TLKINODSAAGAGE---
                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=39947;
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                                                                                                                                                                                                                                              01-OCT-2003
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01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q40215;
01-NOV-1996
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                                                                                                                                                                                                                           07XHP7
                                                                                                                                                                                                      Q7XHP7
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                                                                                                                                                       RESULT 14
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Q40215
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                                                               AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQA----HRKELE 178
                                                                                                                                  - EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQA-----HRKELE 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
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YDYLIKLLLIGDSGVGKSCLLLRFSDGSFTTSFITTIGIDFKIRTIELDGKRIKLQIWDT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0005525; F:GTP binding; IEA.
GO; GO:0003928; F:RAB small monomeric GTPase activity; IEA.
GO; GO:00015031; P:protein transport; IEA.
GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
GO; GO:000160; P:two-component signal transduction system (p. . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borg S., Brandstrup B., Jensen T.J., Poulsen C.; "Identification of new protein species among 33 different small GTP-binding proteins encoded by CDNAs from Lotos japonicus, and expression of corresponding mRNAs in developing root nodules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YDYLIKLLLIGDSGYGKSCLLLRPSDGSFTTSPITTIGIDFKIRTIELDGKRVKLQIWDT
                                          AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant J. 11:237-250(1997).
--- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
--- EMBL; Z73947; CAA9175.1;
--- EMSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.9%; Score 518; DB 10; Deliyer. -48.6%; Pred. No. 4.3e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRPAMS; TIGR00231; small GTP; 1.
PROSTTE; PS00675; SIGWAS4_INTERACT_1; 1.
GTP-binding; Lipoprotein.
SEQUENCE 214 AA; 23627 MW; 5E1A6E83505E50D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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InterPro; IPR002078; Sig54 interact.
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Root nodules;
MEDLINE=97231679; PubMed=9076991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003579; GTPase Rab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
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01,
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192 TIKINQSDQ 200
                                                                                                                                                                                                                           GLRMRASNE 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=34305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lotus japonicus.
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01-NOV-1996 (
01-OCT-2003 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 AGQERFRIITTAYYRGAMGILLVYDVTDESSFNNIRNWIRNIEQHASDNVNKILVGNKAD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 - EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRMR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71
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MEDINE=97231679; PubMed=9076991;
Borg S., Brandstrup B., Jensen T.J., Poulsen C.;
Indentification of new protein species among 33 different small GTP-binding proteins encoded by cDNAs from Lotos japonicus, and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 YDYLIKLLLIGDSGVGKSCLLLRFSDGSFTTSFITTIGIDFKIRTIELDGKRIKLQIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons, core eudicots, rosids,
eurosids I; Fabales, Fabaceae, Papilionoideae, Loteae, Lotus.
                                                                                                                                                                                                  Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki T., Marsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                                                                                                                                                         Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone:P0565A07.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005194; BAC80082.1; -. SEQUENCE 215 AA; 23993 MW; F3DAD303C533C7EE CRC64;
ol-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) Putative ethylene-responsive small GTP-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Cf corresponding mRNAs in developing root nodules.";

Plant J. 11:237-250(1997).

Plant J. 11:237-250(1997).

EMBL; 273944; CAA981D2.1; -.

EMBL; 273944; CAA981D2.1; -.

BR GO; GO:0005255; F:GTP binding; IEA.

GO; GO:0005255; F:GTP binding; IEA.

GO; GO:00012928; F:RAB small monomeric GTPase activity; IEA.

GO; GO:0001201; P:Protein transport; IEA.

GO; GO:0001201; P:Protein transport; IEA.

GO; GO:0001201; P:Protein transport; IEA.

GO; GO:0001201; P:Protein transport; IEA.

GO; GO:0001201; P:Protein transport; IEA.

GO; GO:0001201; P:RMD:01806; Ras_trinsframg.

InterPro; IPR001806; Ras_trinsframg.

InterPro; IPR001806; Ras_trinsframg.

InterPro; IPR001806; Ras_trinsframg.

InterPro; IPR001806; Ras_trinsframg.

InterPro; IPR00407; Ras_1.

RINTS; PR00449; RASTRNSFRMNG.

SWART; SM00175; RAB; 1.

RINTS; PR00449; RASTRNSFRMNG.

SWART; SM00175; RAB; 1.

ROSITE: PS00675; SIGMA54_INTERACT_1; 1.

ROSITE: PS00675; SIGMA54_INTERACT_1; 1.

SGUENCE 216 AA; 23776 MW; S69926CCA8D18489 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 - BEOKROVGREGGOGLAKEYGMDFYETSACTNINIKESFTRLTELVLQAHRKELEGLRMR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIBVDGIKVRIQIWDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
46.7%; Score 515.5; DB 10; Length 216;
Best Local Similarity 48.3%; Pred. No. 7.1e-36;
Matches 100; Conservative 43; Mismatches 57; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 ASNELALAELEEEGKPEGPANSSKTC 210
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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March 21, 2004, 11:58:09; Search time 2486 Seconds (without alignments) 2546.574 Million cell updates/sec
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1105
1 MAKQYDVLFRLLLIGDSGVG......LEBEBGKFEGPANSSKTCWC 212
OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                   BLOSUM62
Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                 Sequence:
                                      Run on:
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55026578 Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Minimum DB seq length: 0 Maximum DB seq length: 2000000000

27513289 segs, 14931090276 residues

Searched:

Listing first 45 summaries

em_estfun:* em_estom:* em_gss_hum:* em gas pro: *
em gas phg: *
em gas vrl: * em_gas_pln:* _fun:* em_gss_mus:* ет двв тат: 1: em_estba:*
2: em_esthum:*
3: em_estin:*
5: em_estpu:*
6: em_estpl:*
7: em_estro:* em_htc:* gb_est1:* gb_est2:* gb_est2:* gb_est4:* gb_est4:* em_gss_vrl gb_gssl:* em gas em gas EST:* Database :

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	

Ř	8		% Query	•		!	•	
	No.	Score	Match	Length	BB :	ID	Description	no
		66		109	10	033	60330	601768
	7	98	9.	8	13	784	17848	AGENCOURT
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	ø	91	ö	σ	10	173	01730	601753464
	۲	910	ö	0	10	816	78163	601809083
	c o	882	ö	σ	12	793	57933	603237549
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	15	846	9	3	14	852	78521	7
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	21	815	ë.	ø	13	3372	33729	Щ
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	30	693.5	'n	7	12	333	3703353	
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	32	99	ċ	S	10	2261	22618	
	36	658.5	o,	σ	10	3768	87683	
	37	653	6	9	13	7688	76887	
	38	651	8	æ	13	5517	55176	
	39	651	8	a	12	1717	17178	
	40	650	φ.	~	13	9699	26967	
	c 41	649	œ.	æ	12	3645	36454	
	42	645	ω.	æ	13	1761	X24761	BY24761
	43	639	57.8	416	13	BY269783	BY269783	BY269783
	44	639	۲.	9	13	5071	6071	BY26071
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ALIGNMENTS

EST 30-OCT-2000	MAGE:3987745 5',						Euteleostomi;	; Murinae; Mus.	
1091 bp mRNA linear EST 30-OCT-2000	ulus cDNA clone I						iata; Vertebrata;	rognathi; Muridae	
1091 bg	AP_Lu29 Mus musc		140541		e mouse)		1; Chordata; Cran	1; Rodentia; Sciu	1)
BF160330	601768601F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3987745 5', mRNA sequence.	BF160330	BF160330.1 GI:11040541	EST.	Mus musculus (house mouse)	Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria	1 (bases 1 to 1091)
	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE

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160 luSerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyL 180
                                                                                                                                                      200 ProGluGlyProAlaAsnSerSerLysThrCysTrpCys 212
                                                                                                                                                                                            676 cccrececcaccaaarcrrcaaagacreccrecrec 714
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Mus musculus"
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/strain="FVB/N-3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
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Mus musculus
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988.00
98.06%
95.63%
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Best Local Similarity:
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TITLE
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COMMENT
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BU517848
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Stem cell origin."
/tlab host="nH108"
/clone lib="NLI_CGAP_Lu29"
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
/blbrary constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 AGCCCAGGGAATATTTTTAGTCTACGACATTAGCAGTGAGCGCTCCTATCAGCATATCAT 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 ATCGGTGTTGACTTTAACGATGAAGACTATCGAAGTAGACGGCATCAAAGTGAGAATACA 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 AAGACATGCCTGCTGTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCATATCTCCACC 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerTHislleSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 ileGlyvalAspPheLys-MetLysThrileGluValAspGlyIleLysValArgIleGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nileTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lound through the I.M.A.G.E. Consortium/LLNL at:
Phttp://image.llnl.gov
Plate: LicAM9195 row: b column: 02
High quality sequence stop: 654.
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-817-198C-2 (1-212) x BF160330 (1-1091)
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996.00
94.42%
92.09%
                                                                                                                                                                                                                                                                                              1. .1091
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Best Local Similarity:
Query Match:
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AUTHORS
TITLE
JOURNAL
COMMENT
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/clone_lib="NLI CGAP Mam2"
/note="Organ: mammary; Vector: pCWV-SPORT6; Site_1: Sal1;
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                                                                      180 euArgMetArgAlaSer-AsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGluGlyLys 199
                                                                                                          153 ATGGCGAAACAGTACGATGTGCTGTTCCGGCTACTGCTGATCGGGGACTCCGGGGTTGGC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 AAGACATGCCTGCTGCTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCATATCTCCACC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 1004)
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"I I (Dasses I to low,")

"National Institutes of Health, Mammalian Gene Collection (MGC)

"Unpublished (1999)

"Contact: Robert Strausberg, Ph.D.

Email: cgapbe-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The Im.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lnl.gov

Plate: LLAM14092 row: h column: 05

High quality sequence stop: 586.
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556 AGTCCTTCACTCGTCTGACGGAGCTGCTGCTGCAGGCCCACAGGAAGAGCTGGATGGTC
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                                                                                                                                                                                                                                                                                                                                                              AGENCOURT 10165969 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:6515476 5', mRNA sequence.
BU517848
BU517848.1 GI:22825374
EST.
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/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site 1: Not!; Site 2: Sali; Cloned unidirectionally. Primer: Oligo dT. Average insert 2: Ab. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI648588 616 bp mRNA linear EST 12-SEP-2001 603277781F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5317917 5', mRNA sequence.
BI648588.1 GI:15562824
                                                                                                                                                                                                                                                                                                                                                                                                                                              81 AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AsnLysAlaAspGluGluGluGlnLysArgGlnValGlyArgGluGlnGlnGlnLeuAla 140
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                                                                                                                                                                                                                                                                                                                     145 ATGGCGAAACAGTACGATGTGCTGTTCCGGCTACTGCTGATCGGGGACTCCGGGGTTGGC 204
                                                                                                                                                                                                                                                                                                                                                                                          205 AAGACATGCCTGCTGTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCATATCTCCACC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgMetArgAla-SerAsnGluLeuAlaLeuAla---GluLeuGluGluGluGluGlyLy 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          445 AAGTGGGTCAGTGACGTGGATGAGTACGCTCCAGAAGGAGTCCAGAAGATCCTAATTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     385 GCCCAGGGAATATTTTTAGTCTACGACATTAGCAGTGAGCGCTCCTATCAGCATATCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
                                                                                                                                                                                                                                                                                                                                                                       LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
                                                                                                                              932
187
9
2
                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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Mus musculus
Eukaryota, Metazoa, Chordata
Mammalia, Eutheria, Rodentia
1 (bases 1 to 616)
                                                                                                                            4.57e-103
953.50
94.63%
91.22%
86.29%
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Best Local Similarity:
                                                                                                           Alignment Scores:
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases I to 932)
NIH-MGC http://mgc.nci.nih.gov/.
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Joffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Likuk at:
http://mage.lln.gov
Plate: LiAM9525 row m column: 09
High quality sequence stop; 685.
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602054039FI NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4193456 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu 180
                                                                                          80
                   9
                                                                                                                                                                                                                                                             453 AAGTGGGTCACTGACGTGGATGAGTACGCTCCAGAAGGAGTCCAGAAGATCCTAATTGGG
                                                                                                                                                                                                                                                                                                                                    633 TCCTTCACTCGTCTGACGGAGCTGGTGCTGCAGGCCCACAGGAAAGAGCTGGATGGTCTC
                                                     Arcegretreactritaacarcaacarcarcraceccarcaaacreacac
                                                                                      IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
                                                                                                                          AlaGlnGlyllePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet
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                                                                                                                                                                                                                                          LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly
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BF535642
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Mus musculus
Mus musculus
                                                     273
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TITLE
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COMMENT
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KEYWORDS
SOURCE
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504

564

180

684

624

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/dev stage="adult"
/dob_host="Dulto"
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/dob_host="Dulto"
/dobhost="Dulto"
/d
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Gallus gallus
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phasianinae; Gallus.
1 (Bases I to 759)
Boardman, P.B., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BU343508
6035230888F1 CSEQCHN68 Gallus gallus cDNA clone ChEST465022 5', mRNA
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                                                                                                                         188 LeuAlaLeuAlaGluCluGluGluGluGlyyyaProGluGlyProAlaAsnSerSer
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Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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Mismatches:
Indels:
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/clone="ChEST465022"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PO Box 88, Manchester, M60 1QD, Tel: 01612008930
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BU343508.1 GI:25851509
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                                                                                                                                                                                                                                                                                            LysThrCysTrpCys 212
                                                                                                                                                                                                                                                                                                                                                                   564 AAGACCTGCTGGTGC 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.16e-98
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Best Local Similarity:
Query Match:
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Pred. No.:
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JOURNAL
MEDLINE
PUBMED
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ORGANISM
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VERSION
KEYWORDS
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AUTHORS
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                                                                                                        Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11806 row: a column: 22

High quality sequence stop: 614.

Location/Qualifiers

1. .616

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//note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
//oco="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
//oco not ructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 AAGACTATCGATGTAGACGGCATCAAAGTGAGAATACAGATTTGGGACACAGCAGGGCAG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 GAGAGGTACCAGACTATCACAAAGCAGTACTATCGGCGGAGCCCA-GGAATATTTTAGTC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 GAGTACGCTCCAGAAGGAGTCCAGAAGATCCTAATTGGGAATAAGGCTGATGAAGAGCAG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 TyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThrArgLeuThrGlu 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 LeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArgMetArgAlaSerAsnGlu 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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providing samples: Gilbert Smith, NIH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGlu-GluGluGlyLysPr 200
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Matches:
Conservative:
Mismatches:
Indels:
Plate: LLAM9177 row: p column: 16
High quality sequence stop: 706.
Location/Qualifiers
                                                                        organism="Mus musculus"
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86.85%
84.98%
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Best Local Similarity:
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Pred. No.:
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Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 992)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
L Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGATGGACTTCTATGAGACCAGTGCCTGCAGCAACATGAACATAAAGGAGTCCTTCACC 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 ArgleuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArgMetArg 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 AlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLysProGluGlyPro 203
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                                                                                                                                                                                                                                                                                                                    182 ACGGCAGGGCAGGCGGTACCAGACCATCACCAAGCAGTACTACCGGCGGGGCACAGGGC 241
                                                                        33
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                                                                                                                                                                                                              44 AspPheLysMetLysThrileGluValAspGlyIleLysValArgileGlnIleTrpAsp 63
                                                                                                                                                                                                                                                                                   83
                                                                     GlnTyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyValGlyLysThrCys
                                                                                           CAGTACGACGTGCTGTTCCGCCTGCTGCTGCTCGGCGACTCGGGGGGGAAGATGTGC
                                                                                                                                          24 LeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThrIleGlyVal
                                                                                                                                                                                                                                                                                 ThralaGlyGlnGluarglyrGlnThrlleThrLyaGlnTyrTyrArgArgAlaGlnGly
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     Gaps:
                                      US-09-817-198C-2 (1-212) x BU343508 (1-759)
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KEYWORDS
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AUTHORS
TITLE
JOURNAL
COMMENT
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BF101730
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/clone lib="NCI CGAP Mam3"
//note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BISS7933 699 bp mRNA linear EST 05-SEP-2001
                                                                                                                                                                                                            149 uThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThrArgLeuThrGluLeuVa 169
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Mus musculus (house mouse)

Mus musculus (bordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 699)

NIH-MGC http://mgc.nci.nih.gov/

National institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11734 row: b column: 13
254 GCTCCAGAAGGAGTCCAGAAGATCCTAATTGGGAATAAGGCTGATGAAGAGCAGAAACGG
                                                                                                                                                                                                                                                                                                                                                              189 aLeullaGluLeuGluGluGluGluGluGlyLysProGluGlyProAlaAsnSerSerLysTh
                                                                                                                                169 lLeuGlnAlaHisArgLysGluLeuGluGlyLeuArgMetArgAlaSerAsnGluLeuAl
                                                                                           130 GlnValGlyArgGluGlnGlyGlnGlnLeuAlaLy8-GluTyrGlyMetAspPheTyrGl
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172
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/lab_host="DH108"
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Conservative:
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/organism="Mus musculus"
/mol type="mRNA"
/strain="129,C57BL/6J,FVB/N"
/db xref="taxon:10090"
/clone="IMAGE:5290284"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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BIS57933
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Ciurognathi; Muridae; Murinae; Mus.

Butheria; Rodentia; Sciurognathi; Muridae; Mus.

St. Int-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Lupublished (19
                                                                   BF178163 902 bp mRNA linear EST 31-OCT-2000
601809083F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4039701 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="texco":10090"
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/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/dev_stage="7 months"
/lab host="0H108"
/clone lib="Null CGAP Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sal1;
/sle 2: Not1; Cloned unidirectionally. Primer: Gligo dT.
Library constructed by Life Technologies Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 IleSerSerGluArgSerTyrGlnHisIleMetLysTrpValSerAspValAspGluTyr 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 ATCGAAGTAGACGGCATCAAAGTGATAATACAGATTTGGGACACAGCAGGGCAGGAGAGGG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
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Matches:
Conservative:
Mismatches:
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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                                                                                                                                                                                       BF178163.1 GI:11056305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.91e-98
910.00
97.28%
96.20%
                                                                                                                                   mRNA sequence.
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Best Local Similarity:
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AUTHORS
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JOURNAL
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            RESULT 7
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/mod_type="mRNA"
/mod_type="mRNA"
/db Aref="taxon:10090"
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/clone lih="MIH MGC 203"
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/clone lih="MIH MGC 203"
/clone lih="MIH MGC 203"
/note="Organ: placenta; Vector: pExpress-1; Site l: EcoRV;
Site 2: Not!; RNA obtained from three placentas from
Site 2: Not!; RNA obtained from three placentas from
Sine 2: Not!; RNA obtained from three placentas from
Sine and kept at -80° for two days before RNA
extraction and purlification (Tri-reagent method). cDNA was
primed using oligo-dT primer:
5'-pGACTGTTCTAGATCGCAGGGCGCCCC(7)25-3' and cloned into
the EcoRV/Not! sites of pExpress-1. Size-selection >lkb
resulted in an average insert size of 1.3 kb. This
primary, microquantiry library is normalized to Cot5
(non-normalized primary library is normalized to Cot5
constructed by Express Genomics (Frederick, MD)."
                                                                                                                                                                                    CK030691 773 bp mRNA linear EST 26-NOV-2003 AGENCOURI 16648788 NIH MGC_203 Mus musculus cDNA clone IMAGE:30787643 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Testitute / NIH
Bldg: 31 Rml0A07 Betheada, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Naryan Bhat
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAMIOO row: g column: 12
High quality sequence stop: 706.
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563 TCTTTCACTCGTCTGACAGAGCTGGTCCTGATGGCTCAAAAGGGAGCTGGAGGGCTTG 622
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 773)
11H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/organism="Mus musculus"
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="XGC-egg" / fores | Scori; Site 2: NotI; cDNA / note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from egg. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end"
                       Sanger Institute

Hinkton, Cambridgeshire, CB10 1SA, UK

Bamail: trop@sanger.ac.uk

Sanger Kenopus tropicalis BST project 2001

TROPICALIS_SEQUENCE ID: TEB9119f07.plkSP6

Sequencing primer: SP6

This sequence is from a Xenopus Gene Collection (XGC) library

CONSTRUCTED Agron M. Zorn.

CDNA was oligo dT primed from Sug of poly A+ RNA from egg.

ECORI-NOIL cut cDNA was then ligated into pCS107 with ECORI at the

S' end and Noil at the 3' end.

Vector: pCS107; Site 1: ECORI; Site_2: NotI

Host: Escherichia coli XL1-blue.

Location/Qualifiers

ree
                                                                                                                                                                                                                                      egg.
EcoRI at t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
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       Contact: Taylor R
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SOURCE Homo sapiens (human) ORGANISM Homo sapiens REFERENCE Homo sapiens REFERENCE I To 796) Authors I to 736) Authors I to 736) Authors I to 736 Contact: Robert Strausberg, Ph.D. Tissue Procurement: Miklos Palkovits, M.D., Ph.D. Command I to 736 Authors I to 736 Contact: Arrayed Palkovits, M.D., Ph.D. Contact: Arrayed by: The 1.M.A.G.E. Consortium (LAML) DNA Sequencing by: Incyte Genomics, Inc. Clond Attroagh the I.M.A.G.E. Consortium/LLNL at: Authors I to 736	Alignment Scores: Pred. No.: Pred. No.: Score: Score: Percent Similarity: 75.70% Matches: 195 Best Local Similarity: 75.00% Mismatches: 14 Query Match: 10 Gaps: 1	US-09-817-198C-2 (1-212) x BF966292 (1-796) QY MetalaLy8GlnTyraspValLeuPheArgLeuLeuLleGlyAspSerGlyValGly 20 ATGGCGAAGCAGTACGATGTGCTGTTCCGGCTGCTGCTGGACTCGGGGTGGGC 69 Ly8ThrCy8LeuLeuCy8ArgPheThrAspAsnGluPheHisSerSerHisIleSerThr 40
AUTHORS Clark.A.G. Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Turk.A.G. Glanowski,S., Nielson,R., Tanomas,P., Kejariwal,A., Tanomabaum,D.M., Civello,D.R., Lu,F., Thurphy,B., Ferriera,S., Wang,G., Zdreg,A.H., White,T.G., Shinsky,J.G., Ferriera,S., Wang,G., Zdreg,A.H., White,T.G., Shinsky,J.G., Ferriera,S., Wang,G., Zdreg,A.H., White,T.G., Shinsky,J.G., This sequence as made by sequencing genomic exons and ordering them Rockville, MD 20050, Uso. COMMENT This sequence as made by sequencing genomic exons and ordering them PEATURES Location/Qualifiers Augusted on alignment. Discontinuous Augusted on alignment. Discontinuous Augusted on alignment cores Augusted on alignm	Oy 103 ValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGlyAsnLys 122 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 143 TyrGlyMetAspPheTyrGluThrSerAlaCysThrAshLeuAshIelysGluSerPhe 162 Db 303 TACGGCATGGACTTCTACGAAACAGCTGCACCTTAATATTAAAGACTCCTTC 362 Oy 163 ThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArgMet 182 Db 363 ACTCGTCTGACGGACTGGTGCAGGACGAGGAAGAGAGTGGATGTTCTGGAACA 422 Oy 183 ArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLysProGluGly Db 423 ACTCGTCTGACGGACGACTGGAGGCCGAGGAGGAGGAGGAACCTGGAGGCAAGCTGGAGGCCAAGCTGGAGGCCAAGCTGGAGGCCGAGGAGGCAAACCTGAGGG Oy 203 ProAlaAshSerSerLysThrCysTrpCys 212 Db 483 CCAGCAAACTCTTCAAAGACTGCTGGTGC 512 RESULT 14 BF966292 LCCUS BF966292 LCCUS BF966292 ACCESSION BF966292.1 GI:12333507 XEXWONDS EST.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 AsnIleLysGluSerPheThr-ArgLeuThrGluLeuValLeuGlnAlaHisArgLys-- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGTGGGTCAGTGACGTGGATGAGGTAGGAGATGCCACCTCACTGCCGGGGTGTGGAGAG 368
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Sattus norvegicus (Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                      369 GGTGCCTCACCGGGGAAGGCAAGGCGAGGGCCAGATGGGAAGGCAAATGCTTCCAGGAAG
                                                                                                                                                                                                                                                                  eleulleGlyAsnLysAlaAspGluGluGluGlnLysArgGlnValGlyArgGluGlnGlyGl
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Plate: 00035 row: b column: 1.
Location/Qualifiers
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/organism="Rattus norvegicus"
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Amgen EST Program.
Amgen Rat EST Program.
Unpublished (2003)
Contact: Dan Fitzpatrick
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                                             136 ArgacaAAcAgracaArgracrarrrcaacracracracrastcaacaacrccaagracac
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